From: Bowman, Amy
Sent: Wednesday, February 09, 2005 9:04 AM
To: STIC-Biotech/ChemLib
Subject: sequence search- ~~10/820,720~~ 10/820820

Please search SEQ ID NO: 4 in application 10/820,820, length limited to 150 nucleotides.
Thank you,
Amy Bowman
AU 1635

CN nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: February 18, 2005, 17:58:16 ; Search time 1454 Seconds
(without alignments)
3165.919 Million cell updates/sec

Title: US-10-820-820-4
Perfect score: 95
Sequence: 1 accguugguuccguagugu........aaacaaagacagucgcuuuu 95

Scoring table: IDENTITY_NUC
            Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422760795 residues

Total number of hits satisfying chosen parameters: 2505164

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Databases : GenEmbl:*
   1: gb_ba:*
   2: gb_htg:*
   3: gb_in:*
   4: gb_om:*
   5: gb_ov:*
   6: gb_pat:*
   7: gb_ph:*
   8: gb_pl:*
   9: gb_pr:*
  10: gb_ro:*
  11: gb_sts:*
  12: gb_sy:*
  13: gb_un:*
  14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	95	100.0	95	6	E33206	E33206 Expression
2	95	100.0	95	6	AX138447	AX138447 Sequence
3	95	100.0	95	6	BD015615	BD015615 Slidable
4	76.8	80.8	132	6	AR041184	AR041184 Sequence
5	76.8	80.8	132	6	AR113038	AR113038 Sequence
6	76.8	80.8	132	6	I66463	I66463 Sequence 17
7	74.8	78.7	88	6	BD143502	BD143502 Nucleic a
8	74.8	78.7	88	6	BD182356	BD182356 Sequence
9	74.8	78.7	88	6	AX453846	AX453846 Sequence
10	74.8	78.7	100	6	E47174	E47174 Method for
11	74.8	78.7	117	6	BD174675	BD174675 Ribozyme
12	74.8	78.7	117	6	BD143601	BD143601 Method of
13	74.8	78.7	137	6	AX429079	AX429079 Sequence
14	74.8	78.7	138	6	AX453858	AX453858 Sequence
15	74.8	78.7	141	6	AX138491	AX138491 Sequence
16	74.8	78.7	141	6	BD015659	BD015659 Slidable
17	74.8	78.7	142	6	AX138488	AX138488 Sequence
18	74.8	78.7	142	6	AX138489	AX138489 Sequence
19	74.8	78.7	142	6	AX138490	AX138490 Sequence
20	74.8	78.7	142	6	AX138492	AX138492 Sequence
21	74.8	78.7	142	6	BD015656	BD015656 Slidable
22	74.8	78.7	142	6	BD015657	BD015657 Slidable
23	74.8	78.7	142	6	BD015658	BD015658 Slidable
24	74.8	78.7	142	6	BD015660	BD015660 Slidable
25	74.4	77.9	128	6	E33205	E33205 Expression
26	73	76.8	136	6	E33203	E33203 Expression
27	73	76.8	142	6	E33204	E33204 Expression
28	72	75.8	75	10	K00256	K00256 Rat liver v
29	71.4	75.2	76	6	AX138490	RATTRV1
30	71.4	75.2	76	9	K00253	RABTRV1 Rabbit Val-
31	71.4	75.2	76	9	K00255	HUMTRV1A Human Val-t
32	71.4	75.2	76	9	K00254	HUMTRV1B Human Val-t
33	71.4	75.2	76	10	K00251	MUSTRV1MJ Mouse myelo
34	71.4	75.2	149	6	K00257	RATTRV1MN Rat ascites
35	68.2	71.8	76	10	E33207	MUSTRV1MN Mouse myelo
36	66.8	70.3	113	6	E33208	E33207 Expression
37	65	69.5	110	6	E33209	E33208 Expression
38	66.8	68.4	73	6	X04821	XLTRNV Xenopus lae
39	60.8	64.0	149	6	M10916	DROTGV3BB Drosophila
40	58.6	61.7	76	3	M25880	DROTRV3B D.melanogas
41	55.4	58.3	76	3	X05082	DROTRV4 D.melanogas
42	47.4	49.9	76	3	X05082	LITRNV Lupin trans
43	41	43.2	76	8	K00250	YSCTRV2B Yeast (S.ce
44	40.4	42.5	74	8	X54513	ATTVAL Arabidopsis
45	37.2	39.2	125	1	X66089	SWTASP S.warneri t

ALIGNMENTS

RESULT 1
E33206

LOCUS   E33206   95 bp   RNA   linear
DEFINITION E33206 Expression system for functional nucleic acid transcription.
ACCESSION   E33206
VERSION   E33206.1   GI:18624000
KEYWORDS   JP 2000069972-A/4.
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 95)
  AUTHORS   Tabira,K., Okawa,A. and Ozeki,S.
  TITLE   Expression system for functional nucleic acid transcription
  JOURNAL   Patent: JP 2000069972-A 4 07-MAR-2000;
            AGENCY OF IND SCIENCE & TECHNOL
COMMENT   Artificial Sequence
            PN   JP 2000069972-A/4
            PD   07-MAR-2000
            PF   31-AUG-1998 JP 1998244755
            PR
            PR
            PI   KAZUNARI TABIRA, ATSUSHI OKAWA, SHIORI OZEKI
            PC   C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC
            PI   C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC
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FEATURES   Location/Qualifiers
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                     /organism="synthetic construct"
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ORIGIN

Query Match   100.0%; Score 95; DB 6; Length 95;
Best Local Similarity   75.8%; Pred. No. 1.1e-21;
Matches 72; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUCCGUAGUGUAGUGGUGUGUAUGGCUGUCGCCUAACACGCGAAAGGUCCCGG 60
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Db   1 ACCGUUGGUUCCGUAGUGUAGUGGUGUGUAUGGCUGUCGCCUAACACGCGAAAGGUCCCGG 60

Qy   61 UUCGAAACCCGGGCCGGAAAAAAGACAGUCGCUUUU 95
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Db   61 ACCGUUGGUUCCGUAGUGUAGUGGUGUGUAUGGCUGUCGCCUAACACGCGAAAGGUCCCGG 60

Db   61 TTCGAAACCGGGCGGGAAACAAAGACAGTCGCTTTT 95

RESULT 2
LOCUS   AX138447   95 bp   RNA   linear   PAT 30-MAY-2001
DEFINITION Sequence 8 from Patent EP1097993.
ACCESSION   AX138447
VERSION   AX138447.1 GI:14274343
KEYWORDS   synthetic construct
SOURCE   synthetic construct
  ORGANISM other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 95)
  AUTHORS   Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
  TITLE   Functional ribozyme chimeric molecules capable of sliding
  JOURNAL   Patent: EP 1097993-A 8 09-MAY-2001;
            Secretary of Agency of Industrial Science and Technology (JP) ;
            Taira, Kazunari (JP) ;
FEATURES   Location/Qualifiers
     source   1..95
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="the nucleotide sequence of the transcript of the
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ORIGIN

Query Match   100.0%; Score 95; DB 6; Length 95;
Best Local Similarity   75.8%; Pred. No. 1.1e-21;
Matches   72; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

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          ||||:||::||||:||||||||||||||||||||||||||||:::||||||||||||||
Db   1 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGG 60

Qy   61 UUCGAAACCGGGCGGGAAACAAAGACAGUCGCUUUU 95
          ::||||||||||||||||||||||||||||||:::::
Db   61 TTCGAAACCGGGCGGGAAACAAAGACAGTCGCTTTT 95

RESULT 3
BD015615
LOCUS   BD015615   95 bp   RNA   linear   PAT 27-AUG-2002
DEFINITION Slidable functional chimeric molecule.
ACCESSION   BD015615
VERSION   BD015615.1 GI:22556752
KEYWORDS   JP 2001190282-A/8.
SOURCE   synthetic construct
  ORGANISM other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 95)
  AUTHORS   Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
  TITLE   Slidable functional chimeric molecule.
  JOURNAL   Patent: JP 2001190282-A 8 17-JUL-2001;
            DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL
            SCIENCE AND MANABU NAKAJIMA TECHNOLOGY, KAZUNARI TAIRA
COMMENT   OS   Artificial Sequence
            PN   JP 2001190282-A/8
            PD   17-JUL-2001
            PF   02-NOV-2000 JP 2000336082
            PI   KAZUNARI TAIRA,MASAKI WARASHINA,TOMOKO KUWABARA,HIROAKI PI
            KAWASAKI
            PC   C12N15/09,A61K31/7105,A61K31/711,A61K38/00,A61K48/00,A61P31/12, PC
            A61P43/00,
            PC   C12N9/22,C12Q1/02,C12Q1/68,G01N33/53,G01N33/566,C12N15/00, PC
            A61K37/02
            CC   Description of Artificial Sequence: the
            nucleotide sequence of
            CC   the
            CC   transcript of the human placental tRNAVal
            FH   Key   Location/Qualifiers

FEATURES   Location/Qualifiers
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FT   /organism='Artificial Sequence'.
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                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"
ORIGIN

Query Match   100.0%; Score 95; DB 6; Length 95;
Best Local Similarity   75.8%; Pred. No. 1.1e-21;
Matches   72; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
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Db   1 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGG 60

Qy   61 UUCGAAACCGGGCGGGAAACAAAGACAGUCGCUUUU 95
          ::||||||||||||||||||||||||||||||:::::
Db   61 TTCGAAACCGGGCGGGAAACAAAGACAGTCGCTTTT 95

RESULT 4
AR041184
LOCUS   AR041184   132 bp   DNA   linear   PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5811275.
ACCESSION   AR041184
VERSION   AR041184.1 GI:5961680
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 132)
  AUTHORS   Wong-Staal,F., Yu,M., Yamada,O., Ojwang,J.O., Leavitt,M. and Ho,A.
  TITLE   HIV-specific ribozymes
  JOURNAL   Patent: US 5811275-A 17 22-SEP-1998;
FEATURES   Location/Qualifiers
     source   1..132
                     /organism="unknown"
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ORIGIN

Query Match   80.8%; Score 76.8; DB 6; Length 132;
Best Local Similarity   75.0%; Pred. No. 1.9e-15;
Matches   60; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
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Db   11 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAACGGTCCCCGG 70

Qy   61 UUCGAAACCGGGCGGGAAACA 80
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Db   71 TTCGAAACCGGGCGGGAAACA 90

RESULT 5
ARI13038
LOCUS   ARI13038   132 bp   DNA   linear   PAT 16-MAY-2001
DEFINITION Sequence 17 from patent US 6132962.
ACCESSION   ARI13038
VERSION   ARI13038.1 GI:14093360
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 132)
  AUTHORS   Wong-Staal,F., Yu,M., Yamada,O., Ojwang,J.O., Leavitt,M.C. and
            Ho,A.
  TITLE   Retroviral vectors comprising an anti-hiv or other nucleic acid
  JOURNAL   Patent: US 6132962-A 17 17-OCT-2000;
FEATURES   Location/Qualifiers
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ORIGIN
                    /mol_type="unassigned DNA"

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Db   11 ACGGUUGGUUUCCGUAGUGUGAUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCCGG 60

Qy   61 UUCGAAACCGGGCGCGGGAAACA 80
            ||||||||||||||||||||||||
Db   71 UUCGAAACCGGGCGCGGGAAACA 90

RESULT 6
I6463

LOCUS   I6463   132 bp   DNA   linear   PAT 28-DEC-1997
DEFINITION Sequence 17 from patent US 5670361.
ACCESSION   I6463
VERSION   I6463.1 GI:2724440
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 132)
  AUTHORS   Wong-Staal,F., Yu,M., Yamada,O., Ojwang,J.O., Leavitt,M.C. and
            Ho,A.
  TITLE   HIV-specific ribozymes
  JOURNAL   Patent: US 5670361-A 17 23-SEP-1997;
FEATURES   Location/Qualifiers
     source   1..132
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ORIGIN

Query Match   80.8%; Score 76.8; DB 6; Length 132;
Best Local Similarity 75.0%; Pred. No. 1.9e-15;
Matches   60; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

Qy   1 ACGGUUGGUUUCCGUAGUGUGAUUACAGGUUCGCCUAACACGCGAAAGGUCCCCGG 60
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Db   11 ACGGUUGGUUUCCGUAGUGUGAUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCCGG 60

Qy   61 UUCGAAACCGGGCGCGGGAAACA 80
            ||||||||||||||||||||||||
Db   71 UUCGAAACCGGGCGCGGGAAACA 90

RESULT 7
BD143502

LOCUS   BD143502   88 bp   RNA   linear   PAT 17-JAN-2003
DEFINITION Nucleic acid enzyme acquiring activity of cleaving other specific
            target RNA by recognizing RNA molecule.
ACCESSION   BD143502
VERSION   BD143502.1 GI:27849260
KEYWORDS   JP 2002119283-A/5.
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 88)
  AUTHORS   Taira,K., Warashina,M. and Warashina,T.
  TITLE   Nucleic acid enzyme acquiring activity of cleaving other specific
            target RNA by recognizing RNA molecule.
  JOURNAL   Patent: JP 2002119283-A 5 23-APR-2002;
            DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL
            SCIENCE AND P T BAKRIE AND BROTHERS,JAPAN BIO INDUSTRY ASSOCIATION,
            TECHNOLOGY
COMMENT   OS   Artificial Sequence
            PN   JP 2002119283-A/5
            PD   23-APR-2002
            PF   13-OCT-2000 JP 2000313320

FEATURES   Location/Qualifiers
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ORIGIN

Query Match   78.7%; Score 74.8; DB 6; Length 88;
Best Local Similarity 70.9%; Pred. No. 9.5e-15;
Matches   61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;

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Qy   61 UUCGAAACCGGGCGCGGGAAACAAAGACA 86
            ::|||||||||||::||||||||||||||
Db   61 UUCGAAACCGGGCCACUACAAAAAACCA 86

RESULT 8
BD182356

LOCUS   BD182356   88 bp   RNA   linear   PAT 15-MAY-2003
DEFINITION Novel maxizyme.
ACCESSION   BD182356
VERSION   BD182356.1 GI:30793274
KEYWORDS   WO 0209282l-A/3.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 88)
  AUTHORS   Taira,K., Warashina,M., Kawasaki,H., Hara,T. and
            Nozawa,I.
  TITLE   Novel maxizyme
  JOURNAL   Patent: WO 0209282l-A 3 21-NOV-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            TAISHO PHARMACEUTICAL CO LTD, GENOFUNCTION INC; KAZUNARI TAIRA,
            TOMOKO WARASHINA,MASAKI WARASHINA,HIROAKI KAWASAKI,TOSHIFUMI HARA,
            IWAO NOZAWA
COMMENT   OS   Homo sapiens (human)
            PN   WO 0209282l-A/3
            PD   21-NOV-2002
            PF   30-APR-2002 WO 2002JP004322
            PR   01-MAY-2001 JP 01P
            PR   01-MAY-2001 JP 2002JP004322 134469
            KAWASAKI,
            PI   TOSHIFUMI HARA,IWAO NOZAWA
            maxizyme
            PC   C12N15/55,C12N9/22,C12Q1/34,A61K48/00,A61K38/43 CC Novel
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            TAISHO PHARMACEUTICAL CO LTD,GENOFUNCTION INC; KAZUNARI TAIRA,
            TOMOKO WARASHINA,MASAKI WARASHINA,HIROAKI KAWASAKI,TOSHIFUMI HARA,
            IWAO NOZAWA
            PI   KAZUNARI TAIRA,MASAKI WARASHINA,TOMOKO WARASHINA PC
                 C12N15/09,A61K9/127,A61K38/46,A61K48/00,A61P31/12,A61P35/00, PC
                 C12N15/19,C12N1/21,C12N5/10,C12N9/00,C12Q1/25,C12Q1/68,C12N15/
                 00,A61K37/54,
            PC   C12N1/15,
            PC   C12N5/00
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ORIGIN

Query Match   78.7%; Score 74.8; DB 6; Length 88;
Best Local Similarity 70.9%; Pred. No. 9.5e-15;
Matches   61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;

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RESULT 9
LOCUS       AX453846                  88 bp    RNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 5 from Patent EP1213351.
ACCESSION   AX453846
VERSION     AX453846.1  GI:21713515
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Taira,K., Warashina,M. and Warashina,T.
  TITLE     Nucleic acid enzymes acquiring an activity for cleaving a target
            rna by recognizing another molecule
  JOURNAL   Patent: EP 1213351-A 5 12-JUN-2002;
            National Institute of Advanced Industrial Science and Technology
            (JP)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="tRNAVal promoter sequence"
ORIGIN

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Db          1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCCGG 60

Qy         61 UUCGAAACCCGGGCGGGAAACAAAAGACA 86
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Db         61 UUCGAAACCCGGGCACUACAAAAACCA 86
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RESULT 10
LOCUS       E47174                   100 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for selecting active ribozyme.
ACCESSION   E47174
VERSION     E47174.1  GI:22553362
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Tabira,K. and Kawasaki,H.
  TITLE     Method for selecting active ribozyme
  JOURNAL   Patent: JP 2001128682-A 9 15-MAY-2001;
            AGENCY OF IND SCIENCE & TECHNOL
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001128682-A/9
            PD   15-MAY-2001
            PF   05-NOV-1999 JP 199931579
            PI   KAZUNARI TABIRA,HIROAKI KAWASAKI
            PC   C12N15/09,C12Q1/68//C12N15/10,C12N15/00,C12N5/00 CC
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            FEATURES             Location/Qualifiers
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Query Match   78.7%; Score 74.8; DB 6; Length 100;
Best Local Similarity 70.9%; Pred. No. 9.5e-15;
Matches 61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;

ORIGIN

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Db          1 ACCGTTGGTTTCCGTAGTGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAAGGTCCCCGG 60

Qy         61 UUCGAAACCCGGGCGGGAAACAAAAGACA 86
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Db         61 TTCGAAACCCGGGCACTACAAAAACCA 86
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RESULT 11
LOCUS       BD174675                 117 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Ribozyme expression system.
ACCESSION   BD174675
VERSION     BD174675.1  GI:29120365
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 117)
  AUTHORS   Takebe,Y. and Okawa,J.
  TITLE     Ribozyme expression system
  JOURNAL   Patent: JP 2002262880-A 1 17-SEP-2002;
            DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIOUS DISEASES,
            YUTAKA TAKEBE,JUN OKAWA
COMMENT     OS   Artificial Sequence
            PN   JP 2002262880-A/1
            PD   17-SEP-2002
            PF   09-MAR-2001 JP 2001067253
            PI   YUTAKA TAKEBE,JUN OKAWA
            PC   C12N15/09,A61K31/711,A61K35/76,A61K48/00,A61P31/18,C12N5/10,
            PC   C12N9/00,
            PC   C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: the nucleotide sequence of
            CC   tetO1-tRNAVal
            FH   Key                    Location/Qualifiers
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                     /organism="synthetic construct"
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Query Match   78.7%; Score 74.8; DB 6; Length 117;
Best Local Similarity 70.9%; Pred. No. 9.5e-15;
Matches 61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;

ORIGIN

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Db          1 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAAGGTCCCCGG 60

Qy         61 UUCGAAACCCGGGCGGGAAACAAAAGACA 86
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Db         61 TTCGAAACCCGGGCACTACAAAAACCA 86
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RESULT 12
LOCUS       BD143601                 137 bp    RNA     linear   PAT 17-JAN-2003
DEFINITION  Method of selecting high-function nucleic acid molecule in cell.
ACCESSION   BD143601
VERSION     BD143601.1  GI:27849359
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Query Match   78.7%; Score 74.8; DB 6; Length ;
Best Local Similarity 70.9%; Pred. No. 9.5e-15;
Matches 61; Conservative 18; Mismatches 7; Indels 0; Gaps 0;

ORIGIN

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              ||||||:||:||||||:::||||||||||||||||||||||||||||||||||||||||||
Db         29 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAAGGTCCCCGG 88

Qy         61 UUCGAAACCCGGGCGGGAAACAAAAGACA 86
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Db         89 TTCGAAACCCGGGCACTACAAAAACCA 114
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KEYWORDS   .
SOURCE   synthetic construct
  ORGANISM   synthetic construct
             other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 137)
  AUTHORS   Taira,K. and Sano,M.
  TITLE   Method of selecting high-function nucleic acid molecule in cell
  JOURNAL   Patent: JP 2002125685-A 2 08-MAY-2002;
             DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL
             SCIENCE AND HIROSHI YATSUHASHI, TECHNOLOGY, KAZUNARI TAIRA
  OS   Artificial Sequence
COMMENT   PN   JP 2002125685-A/2
             PD   08-MAY-2002
             PF   30-OCT-2000 JP 2000331347
             PR
             PI   KAZUNARI TAIRA, MASAYUKI SANO
             PC   C12N15/09,C12N9/00,C12Q1/02,C12Q1/68,C12N15/00 CC
                  C12N15/09,C12N9/00,C12Q1/25,C12Q1/68,C12N15/00 CC
             Description of Artificial Sequence: Sequence of tRNA-Luc GUA CC
             Rz
FEATURES   Location/Qualifiers
     FH   Key
     FT   source   1..137
     FT   /organism="Artificial Sequence".
ORIGIN

Query Match   78.7%; Score 74.8; DB 6; Length 137;
Best Local Similarity   70.9%; Pred. No. 9.5e-15;
Matches   61; Conservative   18; Mismatches   7; Indels   0; Gaps   0;

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Qy   61 UUCGAAAACCGGGCGGCCGAAAACAAAAGACA 86
              |||||||||||||||||| | || |||||
Db   61 TTCGAAAACCGGGCGGCCGACTACAAAAAACCA 86

RESULT 13
LOCUS   AX429079   137 bp   RNA   linear   PAT 21-JUN-2002
DEFINITION Sequence 2 from Patent EP1201751.
ACCESSION   AX429079
VERSION   AX429079.1 GI:21540419
KEYWORDS   .
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Taira,K. and Sano,M.
  TITLE   Method for selecting highly functional nucleic acid molecules
            within cells
  JOURNAL   Patent: EP 1201751-A 2 02-MAY-2002;
            National Institute of Advanced Industrial Science and Technology
            (JP)
FEATURES   Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Sequence of tRNA-Luc GUA Rz"
ORIGIN

Query Match   78.7%; Score 74.8; DB 6; Length 137;
Best Local Similarity   70.9%; Pred. No. 9.5e-15;
Matches   61; Conservative   18; Mismatches   7; Indels   0; Gaps   0;

Qy   1 ACCGGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
              ||||:|::||||:||||::|:|||:||:|||||||||:|||||||||||||||||||||||
Db   1 ACCGGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGG 60

Qy   61 UUCGAAAACCGGGCGGCCGAAAACAAAAGACA 86
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Db   61 TTCGAAAACCGGGCGGCCGACTACAAAAAACCA 86

RESULT 14
LOCUS   AX453858   138 bp   RNA   linear   PAT 06-JUL-2002
DEFINITION Sequence 17 from Patent EP1213351.
ACCESSION   AX453858
VERSION   AX453858.1 GI:21713527
KEYWORDS   .
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Taira,K., Warashina,M. and Warashina,T.
  TITLE   Nucleic acid enzymes acquiring an activity for cleaving a target
            rna by recognising another molecule
  JOURNAL   Patent: EP 1213351-A 17 12-JUN-2002;
            National Institute of Advanced Industrial Science and Technology
            (JP)
FEATURES   Location/Qualifiers
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                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="tRNAVal T-MzL"
ORIGIN

Query Match   78.7%; Score 74.8; DB 6; Length 138;
Best Local Similarity   70.9%; Pred. No. 9.5e-15;
Matches   61; Conservative   18; Mismatches   7; Indels   0; Gaps   0;

Qy   1 ACCGGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
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Db   1 ACCGGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGG 60

Qy   61 UUCGAAAACCGGGCGGCCGAAAACAAAAGACA 86
              |||||||||||||||||| | || |||||
Db   61 TTCGAAAACCGGGCGGCCGACTACAAAAAACCA 86

RESULT 15
LOCUS   AX138491   141 bp   RNA   linear   PAT 30-MAY-2001
DEFINITION Sequence 52 from Patent EP1097993.
ACCESSION   AX138491
VERSION   AX138491.1 GI:14274387
KEYWORDS   .
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
  TITLE   Functional ribozyme chimeric molecules capable of sliding
  JOURNAL   Patent: EP 1097993-A 52 09-MAY-2001;
            Secretary of Agency of Industrial Science and Technology (JP) ;
            Taira, Kazunari (JP)
FEATURES   Location/Qualifiers
     source   1..141
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="the nucleotide sequence of CPP Rz4"
ORIGIN

Query Match   78.7%; Score 74.8; DB 6; Length 141;
Best Local Similarity   70.9%; Pred. No. 9.4e-15;
Matches   61; Conservative   18; Mismatches   7; Indels   0; Gaps   0;

Qy   1 ACCGGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60

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Qy     61  UUCGAAACCGGGGCGGGAAACAAAGACA  86
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Db     61  TTCGAAACCGGGGCGACTACAAAAACCA  86
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Search completed: February 18, 2005, 22:02:39
Job time : 1459 secs

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: February 18, 2005, 21:07:17 ; Search time 98 Seconds
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Title:
Perfect score: 95
Sequence: 1 accguugguuccguaguguu..........aaacaaagacagucgcuuuu 95

Scoring table: IDENTITY_NUC
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Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 1367770

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	95	100.0	95	4	US-09-763-590-4	Sequence 4, Appli
2	79	83.2	133	5	PCT-US94-05700-17	Sequence 17, Appl
3	76.8	80.8	132	1	US-08-245-742A-17	Sequence 17, Appl
4	76.8	80.8	132	1	US-08-465-483-17	Sequence 17, Appl
5	76.8	80.8	132	1	US-08-876-996-17	Sequence 17, Appl
6	74	77.9	128	4	US-09-763-590-3	Sequence 3, Appli
7	73	76.8	135	4	US-09-763-590-1	Sequence 1, Appli
8	73	76.8	141	4	US-09-763-590-2	Sequence 2, Appli
9	69.8	73.5	149	4	US-09-763-590-5	Sequence 5, Appli
10	66.8	70.3	113	4	US-09-763-590-7	Sequence 7, Appli
11	66	69.5	110	4	US-09-763-590-6	Sequence 6, Appli
12	25	26.3	106	4	US-09-763-590-13	Sequence 13, Appl
13	25	26.3	109	4	US-09-763-590-12	Sequence 12, Appl
14	23	24.2	81	4	US-09-355-221-6	Sequence 6, Appli
15	22.4	23.6	24	4	US-09-563-794B-71	Sequence 71, Appl
16	22.2	23.4	149	1	US-08-513-999C-10149	Sequence 10149, A
17	21.8	22.9	86	4	US-08-447-169A-212	Sequence 212, Appl
18	21.8	22.9	86	4	US-08-860-474-212	Sequence 212, App
19	21.8	22.9	66	4	US-09-513-390-10	Sequence 10, App
20	21	22.1	64	4	US-09-270-767-29068	Sequence 29068, A
21	21	22.1	78	4	US-09-715-858-9	Sequence 9, Appli
22	20.4	21.5	93	2	US-08-785-750-7	Sequence 7, Appli
23	20.4	21.5	94	3	US-09-121-162-1	Sequence 1, Appli
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32	20.2	21.3	77	1	US-08-345-623-2	Sequence 2, Appli
33	20.2	21.2	101	3	US-09-763-590-11	Sequence 11, Appl
34	19.2	20.2	67	3	US-09-025-769B-74	Sequence 74, Appl
35	19.2	20.2	67	4	US-09-490-070A-74	Sequence 74, Appl
36	19.2	20.2	67	4	US-09-490-153-74	Sequence 74, Appl
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44	18.6	19.6	44	4	US-09-821-167-2	Sequence 2, Appl
45	18.4	19.4	108	3	US-09-284-627-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-763-590-4

; Sequence 4, Application US/09763590
; Patent No. 6740750
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
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; SEQ ID NO 4
; LENGTH: 95
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence of the transcript of human placental tRNA Val
US-09-763-590-4

Query Match   100.0%; Score 95; DB 4; Length 95;
Best Local Similarity   100.0%; Pred. No. 1.9e-27;
Matches   95; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAAACACGCGAAAGGUCCCCG 60

Qy   61 UUCGAAACCGGGCGGGAAACAAAGACAGUCGCUUUU 95
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RESULT 2
PCT-US94-05700-17

; Sequence 17, Application PCT/US9405700
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: RIBOZYME GENE THERAPY FOR HIV INFECTION AND AIDS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBBINS, BERLINER & CARSON

STREET: 201 NORTH FIGUEROA STREET
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05700
FILING DATE: 17 MAY 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BERINER, ROBERT
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: misc_feature
LOCATION: 97
OTHER INFORMATION: /note= "w = INTERNAL NUCLEOTIDE
OTHER INFORMATION: SEQUENCE""
PCT-US94-05700-17

Query Match   83.2%;   Score 79; DB 5; Length 133;
Best Local Similarity 67.4%;   Pred. No. 3.7e-21;
Matches 64; Conservative 21; Mismatches 10; Indels 0; Gaps 0;

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RESULT 3
US-08-245-742A-17
Sequence 17, Application US/0824574 2A
Patent No. 5670361
GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie
APPLICANT: Yu, Mang
APPLICANT: Yamada, Osamu
APPLICANT: Ojwang, Joshua O.
APPLICANT: Leavitt, Mark
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
TITLE OF INVENTION: and AIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,742A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,465
FILING DATE: 17-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 2307E-567-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: (96^97)
OTHER INFORMATION: /note= "insertion location of
OTHER INFORMATION: foreign gene in pol III
OTHER INFORMATION: transcription cassette in
OTHER INFORMATION: vector pMJT"
US-08-245-742A-17

Query Match   80.8%;   Score 76.8; DB 1; Length 132;
Best Local Similarity 75.0%;   Pred. No. 2.7e-20;
Matches 60; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

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Db  71 TTCGAAACCGGGCCGGGAAAACA 90
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RESULT 4
US-08-465-483-17
Sequence 17, Application US/08465483
Patent No. 5811275
GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie
APPLICANT: Yu, Mang
APPLICANT: Yamada, Osamu
APPLICANT: Ojwang, Joshua O.
APPLICANT: Leavitt, Mark
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
TITLE OF INVENTION: and AIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,483
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/062,465
  FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/245,742
  FILING DATE: 17-MAY-1994
ATTORNEY/AGENT INFORMATION:
  NAME: Weber, Kenneth A.
  REGISTRATION NUMBER: 31,677
  REFERENCE/DOCKET NUMBER: 2307E-567-11
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 543-9600
  TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 132 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA
  FEATURE:
    NAME/KEY: -
    LOCATION: (96^97)
    OTHER INFORMATION: /note= "insertion location of
    OTHER INFORMATION: foreign gene in pol III
    OTHER INFORMATION: transcription cassette in
    OTHER INFORMATION: vector pMJT"
US-08-465-483-17

Query Match   80.8%; Score 76.8; DB 1; Length 132;
Best Local Similarity   75.0%; Pred. No. 2.7e-20;
Matches 60; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

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Db   71 TTCGAAACCGGGCGGGAAACA 90
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RESULT 5
US-08-876-996-17
; Sequence 17, Application US/08876996
; Patent No. 6132962
; GENERAL INFORMATION:
  APPLICANT: Wong-Staal, Flossie
  APPLICANT: Yu, Mang
  APPLICANT: Yamada, Osamu
  APPLICANT: Ojwang, Joshua O.
  APPLICANT: Leavitt, Mark
  APPLICANT: Ho, Anthony
  TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
                      and AIDS
  NUMBER OF SEQUENCES: 18
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew
    STREET: One Market Plaza, Steuart Street Tower
    CITY: San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94105-1492
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/876,996
    FILING DATE:
  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,742
  FILING DATE:
ATTORNEY/AGENT INFORMATION:
  NAME: Weber, Kenneth A.
  REGISTRATION NUMBER: 31,677
  REFERENCE/DOCKET NUMBER: 2307E-567-10
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 543-9600
  TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 132 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  MOLECULE TYPE: DNA
  FEATURE:
    NAME/KEY: -
    LOCATION: (96^97)
    OTHER INFORMATION: /note= "insertion location of
    OTHER INFORMATION: foreign gene in pol III
    OTHER INFORMATION: transcription cassette in
    OTHER INFORMATION: vector pMJT"
US-08-876-996-17

Query Match   80.8%; Score 76.8; DB 3; Length 132;
Best Local Similarity   75.0%; Pred. No. 2.7e-20;
Matches 60; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

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Qy    1 ACGGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCACGCCGUAAACGCCGAAAGGUCCCCGG 60
          ||||||:|||::|||:||||||:||||:|:|||:||||||||||::||||| |||||||||||
Db   11 ACGGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCACGCCGAAACGGTCCCGG 70

Qy   61 UUICGAAACCCGGCGGGAAACA 80
           :||||||||||::||||||||
Db   71 TTCGAAACCGGGCGGGAAACA 90
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RESULT 6
US-09-763-590-3
; Sequence 3, Application US/09763590
; Patent No. 6740750
; GENERAL INFORMATION:
  APPLICANT: TAIRA, KAZUNARI
  APPLICANT: OHKAWA, JUN
  APPLICANT: KOSEKI, SHIORI
  TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
  TITLE OF INVENTION: NUCLEIC ACIDS
  FILE REFERENCE: 04853.0059-00000
  CURRENT APPLICATION NUMBER: US/09/763,590
  CURRENT FILING DATE: 2001-06-05
  PRIOR APPLICATION NUMBER: PCT/JP99/04718
  PRIOR FILING DATE: 1999-08-31
  PRIOR APPLICATION NUMBER: JP 10/244755
  PRIOR FILING DATE: 1998-08-31
  NUMBER OF SEQ ID NOS: 25
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 3
    LENGTH: 128
    TYPE: RNA
    ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
    OTHER INFORMATION: sequence of Rz1
US-09-763-590-3

Query Match   77.9%; Score 74; DB 4; Length 128;
Best Local Similarity   93.9%; Pred. No. 3.3e-19;
Matches 77; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy    1 ACGGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCACGCCGUAAACACGCGGAAAGGUCCCCGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ACGGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCACGCCGUAAACACGCGGAAAGGUCCCCGG 60
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Qy  61 UUCGAAACCGGGCGCGGAAACAAA 82
Db  61 UUCGAAACCGGGCGCACCCACACA 82
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RESULT 7
US-09-763-590-1
; Sequence 1, Application US/09763590
; Patent No. 6740750
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 135
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence of Rz2
US-09-763-590-1

Query Match   76.8%; Score 73; DB 4; Length 135;
Best Local Similarity 93.8%; Pred. No. 8.1e-19;
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAAACACGCGAAAGGUCCCCGG 60
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Db   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAAACACGCGAAAGGUCCCCGG 60

Qy  61 UUCGAAACCGGGCGCGGAAACAA 81
       |||||||||||||
Db  61 UUCGAAACCGGGCCACUACAAA  81
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RESULT 8
US-09-763-590-2
; Sequence 2, Application US/09763590
; Patent No. 6740750
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 141
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence of Rz3

US-09-763-590-2

Query Match   76.8%; Score 73; DB 4; Length 141;
Best Local Similarity 93.8%; Pred. No. 8.3e-19;
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAAACACGCGAAAGGUCCCCGG 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAAACACGCGAAAGGUCCCCGG 60

Qy  61 UUCGAAACCGGGCGCGGAAACAA 81
       |||||||||||||
Db  61 UUCGAAACCGGGCCACUACAAA  81
```

RESULT 9
US-09-763-590-5
; Sequence 5, Application US/09763590
; Patent No. 6740750
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 149
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence of Rz4
US-09-763-590-5

Query Match   73.5%; Score 73; DB 4; Length 149;
Best Local Similarity 97.3%; Pred. No. 1.5e-17;
Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAAACACGCGAAAGGUCCCCGG 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAAACACGCGAAAGGUCCCCG  60

Qy  61 UUCGAAACCCGGC 73
       |||||||||||||
Db  61 UUCGAAACCCGGC 73
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RESULT 10
US-09-763-590-7/c
; Sequence 7, Application US/09763590
; Patent No. 6740750
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 7
; LENGTH: 113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of an
; Patent No. 6740750
; OTHER INFORMATION: antisense oligonucleotide linker
US-09-763-590-7

Qy   1 ACGGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAAGGUUCCCCG 60
              ||||||:||:::::|||::|::|||:|||:|:||:::||||:||:||:|||||||||||||
Db   71 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAAGGUUCCCCG 12

Qy   61 UUCGAAACCG 70
              |:|||||:||
Db   11 UUCGAAGUCG 2

RESULT 11
US-09-763-590-6
Sequence 6, Application US/09763590
Patent No. 6740750
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 6
; LENGTH: 110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
; Patent No. 6740750
; OTHER INFORMATION: sense oligonucleotide linker
US-09-763-590-6

Query Match   69.5%; Score 66; DB 4; Length 110;
Best Local Similarity   72.7%; Pred. No. 4.1e-16;
Matches   48; Conservative 18; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ACGGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAAGGUUCCCCG 60
              |:|||:||::||:|||:::::|::|||:|:||||:::||||:||::|:|||||||||||||
Db   44 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAAGGUUCCCCG 103

Qy   61 UUCGAA 66
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Db   104 TTCGAA 109

RESULT 12
US-09-763-590-13/c
Sequence 13, Application US/09/763590
Patent No. 6740750
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI

; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 13
; LENGTH: 106
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
; Patent No. 6740750
; OTHER INFORMATION: lower primer including the sequences of Rz3 and a
; OTHER INFORMATION: terminator
US-09-763-590-13

Query Match   26.3%; Score 25; DB 4; Length 106;
Best Local Similarity   88.0%; Pred. No. 4.2;
Matches   22; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

Qy   49 AAAGGUCCCCGGGUUCGAAAACCGGGC 73
              |||||||||||:|||||||||||||||
Db   106 AAAGGTCCCCGGTTCGAAAACCGGGC 82

RESULT 13
US-09-763-590-12/c
Sequence 12, Application US/09763590
Patent No. 6740750
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/09/763,590
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 12
; LENGTH: 109
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of a
; Patent No. 6740750
; OTHER INFORMATION: lower primer including the sequences of Rz2 and a
; OTHER INFORMATION: terminator
US-09-763-590-12

Query Match   26.3%; Score 25; DB 4; Length 109;
Best Local Similarity   88.0%; Pred. No. 4.2;
Matches   22; Conservative   3; Mismatches   0; Indels   0; Gaps   0;

Qy   49 AAAGGUCCCCGGGUUCGAAAACCGGGC 73
              |||||||||||:|||||||||||||||
Db   109 AAAGGTCCCCGGTTCGAAAACCGGGC 85

RESULT 14

US-09-355-221-6/c
; Sequence 6, Application US/09355221
; Patent No. 6605429
; GENERAL INFORMATION:
; APPLICANT: Barber, Jack
; APPLICANT: Welch, Peter
; APPLICANT: Yei, Soonpin
; APPLICANT: Tritz, Richard
; APPLICANT: Immusol Incorporated
; TITLE OF INVENTION: Gene Functional Analysis and Discovery Using Randomized or
; TITLE OF INVENTION: Target-Specific Ribozyme Gene Vector Libraries
; FILE REFERENCE: 016556-0030US
; CURRENT APPLICATION NUMBER: US/09/355,221
; CURRENT FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/037,352
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: WO PCT/US98/01196
; PRIOR FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 2.1
;
; SEQ ID NO 6
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:tRNA-ribozyme lib
; OTHER INFORMATION: PCR primer (tRNA-Rz lib primer)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(81)
; OTHER INFORMATION: n = g, a, c or t
US-09-355-221-6

Qy
Db

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Query Match             24.2%;  Score 23;  DB 4;  Length 81;
Best Local Similarity   91.3%;  Pred. No. 23;
Matches   21;  Conservative   2;  Mismatches   0;  Indels   0;  Gaps   0;

Qy         58 CGGUUCGAAACCGGGCGGGAAACA 80
              |||:||||||||||||||||||||
Db         81 CGGTTCGAAACCGGGCGGGAAACA 59
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RESULT 15
US-09-563-794B-71
; Sequence 71, Application US/09563794B
; Patent No. 6808876
; GENERAL INFORMATION:
; APPLICANT: KRUGER, MARTIN
; APPLICANT: WELCH, PETER J.
; APPLICANT: BARBER, JACK R.
; TITLE OF INVENTION: CELLULAR REGULATORS OF INFECTIOUS AGENTS AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 039316-0801
; CURRENT APPLICATION NUMBER: US/09/563,794B
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 71
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-563-794B-71

Qy
Db

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Query Match             23.6%;  Score 22.4;  DB 4;  Length 24;
Best Local Similarity   70.8%;  Pred. No. 26;
Matches   17;  Conservative   6;  Mismatches   1;  Indels   0;  Gaps   0;

Qy         24 GGUUAUCACGUUCGCCUAACACGC 47
              ||:::|:|:|||||:|||||||||
Db          1 GGTTATCACGTTCGCCTCACACGC 24
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OM nucleic - nucleic acid search, using sw model

GenCore version 5.1.6
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Run on: February 18, 2005, 21:38:28 ; Search time 253 Seconds
(without alignments)
235.207 Million cell updates/sec

Title: US-10-820-820-4
Perfect score: 95
Sequence: 1 accguuguuccguaggu.........aaacaaagacagucgcuuuu 95.

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 5148868 seqs, 313196961 residues

Total number of hits satisfying chosen parameters:　10002998

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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8: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq2:*
9: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	21.8	22.9	78	6	US-10-932-182A-166715	Sequence 166715
c 2	18.8	19.8	77	6	US-10-605-923-15457	Sequence 15457, A
c 3	18.4	19.4	117	6	US-10-932-182A-174531	Sequence 174531,
c 4	18.2	19.2	103	7	US-10-605-923-10887	Sequence 10887, A
c 5	18.2	19.2	103	7	US-10-605-924-7522	Sequence 7522, Appl
c 6	18	18.9	95	8	US-11-043-312-11	Sequence 11, Appl
c 7	18	18.9	117	6	US-10-707-003-1264	Sequence 1264, Ap
c 8	18	18.9	117	6	US-10-604-984-1264	Sequence 1264, Ap
c 9	17.8	18.7	100	6	US-10-153-469A-3	Sequence 3, Appli
c 10	17.8	18.7	96	6	US-10-932-182A-173417	Sequence 173417,
c 11	17.6	18.5	104	7	US-10-605-923-13759	Sequence 13759, A
c 12	17.6	18.5	104	7	US-10-605-924-9585	Sequence 9585, Ap
c 13	17.6	18.5	112	6	US-11-021-016-12	Sequence 12, Appl
c 14	17.4	18.5	112	6	US-10-605-923-17798	Sequence 17798, A
c 15	17.4	18.3	66	7	US-10-605-924-12307	Sequence 12307, A
c 16	17.4	18.3	96	7	US-10-604-945-1471	Sequence 1471, Ap
c 17	17.4	18.3	147	6	US-10-932-182A-78301	Sequence 78301, A
c 18	17.4	18.3	96	7	US-10-036-317-439867	Sequence 439867,
c 19	17.4	18.3	25	8	US-10-708-952A-397923	Sequence 397923,
c 20	17.2	18.1	60	6	US-11-036-317-439923	Sequence 439923,
c 21	17.2	18.1	60	7	US-10-604-945-3007	Sequence 3007, Ap
c 22	17.2	18.1	65	7	US-10-708-952A-36290	Sequence 36290, A
c 23	17.2	18.1	73	7	US-10-708-952A-388244	Sequence 388244,
c 24	17.2	18.1	82	7	US-10-604-985-809	Sequence 809, App
c 25	17.2	18.1	106	7	US-10-605-923-28491	Sequence 28491, A
c 26	17.2	18.1	106	7	US-10-605-924-19523	Sequence 19523, A
c 27	17.2	18.1	110	8	US-11-031-175-8522	Sequence 8522, Ap
c 28	17.2	18.1	117	8	US-10-708-952A-399286	Sequence 399286,
c 29	17.2	18.1	144	8	US-11-043-770-4	Sequence 4, Appli
c 30	17.2	18.1	144	5	US-09-581-528E-20	Sequence 20, Appl
c 31	17	18.1	36	5	US-11-043-770-992	Sequence 992, Appl
c 32	17	17.9	60	7	US-10-708-952A-390279	Sequence 390279,
c 33	17	17.9	85	7	US-10-605-923-6458	Sequence 6458, Ap
c 34	17	17.9	90	7	US-10-605-923-25873	Sequence 25873, A
c 35	17	17.9	90	7	US-10-605-923-3531	Sequence 3531, Ap
c 36	17	17.9	107	7	US-10-932-182A-81069	Sequence 81069, A
c 37	17	17.9	111	7	US-10-605-923-20831	Sequence 20831, A
c 38	16.8	17.7	130	7	US-10-605-924-14335	Sequence 14335, A
c 39	16.8	17.7	130	6	US-10-605-923-2534	Sequence 2534, Ap
c 40	16.8	17.7	60	6	US-10-708-952A-390279	Sequence 390279,
c 41	16.8	17.7	63	7	US-10-605-923-16921	Sequence 16921, A
c 42	16.8	17.7	63	7	US-10-605-924-11708	Sequence 11708, A
c 43	16.8	17.7	65	7	US-10-605-923-5866	Sequence 5866, Ap
c 44	16.8	17.7	65	7	US-10-605-924-4049	Sequence 4049, Ap
c 45	16.8	17.7	130	6	US-10-708-952A-396673	Sequence 396673,

ALIGNMENTS

RESULT 1
US-10-932-182A-166715/c
; Sequence 166715, Application US/10932182A
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166715
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-166715

Query Match 22.9%; Score 21.8; DB 6; Length 78;
Best Local Similarity 43.8%; Pred. No. 38;
Matches 32; Conservative 9; Mismatches 32; Indels 0; Gaps 0;

```
Qy   8 GUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCCCGGUUCGAAA 67
         |  ||||  || | ||  | |  | |  |||  | :  | |||||  |: |||| |:|
Db  73 GCTTCAGTAGCTCAGTCGGGCGAGAGGCGGTCAGTCTCATAATCTGAAGGTCGAGAGTTCGAAC 14
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RESULT 2
US-10-605-923-15457/c
; Sequence 15457, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15457

```
Qy  68 CCGGGCGGAAACA 80
          | | | |
Db  13 CTCCCCTGGGAGCA 1
```

; LENGTH: 77
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-15457

Query Match   19.8%; Score 18.8; DB 7; Length 77;
Best Local Similarity   45.7%; Pred. No. 5.1e+02; Mismatches 17; Indels 0; Gaps 0;
Matches 21; Conservative 8;

```
Qy    16 AGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGGU 61
         ||:|| || |||||:||| ||||| ||||||| | |:|||||  :|
Db    47 AGCGTTGCCATTATCACCTTTGCCTCAGAGCCCAAAAGTCCTCATGT 2
```

RESULT 3
US-10-932-182A-174531
Sequence 174531, Application US/10932182A
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 174531
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-174531

Query Match   19.4%; Score 18.4; DB 6; Length 117;
Best Local Similarity   56.8%; Conservative 3; Mismatches 16; Indels 0; Gaps 0;
Matches 25;

```
Qy    30 CACGUUCGCCUAACACGCGGAAAGGUCCCCGGUUCGGAAACCGGGC 73
         |||  ||| ||||||||||  ||||||  |:|||||||  |||||
Db    54 CAGGTATGCAAAGCATGCGAGAGCCCTCGGTTCAATTCCCAGC 97
```

RESULT 4
US-10-605-923-10887
Sequence 10887, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10887
; LENGTH: 103
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-10887

Query Match   19.2%; Score 18.2; DB 7; Length 103;
Best Local Similarity   44.7%; Pred. No. 9e+02; Mismatches 18; Indels 0; Gaps 0;
Matches 21; Conservative 8;

```
Qy     8 GUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGU 54
         |:|| |:|||||||||||| || ||| ||||| |: ||| : || ||
Db    21 GATTCTGGACTGAAATGGTATGCAGGTATGACTTAAAAGCCATAGGT 67
```

RESULT 5
US-10-605-924-7522

Sequence 7522, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7522
; LENGTH: 103
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-7522

Query Match   19.2%; Score 18.2; DB 7; Length 103;
Best Local Similarity   44.7%; Pred. No. 9e+02; Mismatches 18; Indels 0; Gaps 0;
Matches 21; Conservative 8;

```
Qy     8 GUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGU 54
         |:|| |:|||||||||||| || ||| ||||| |: ||| : || ||
Db    21 GATTCTGGACTGAAATGGTATGCAGGTATGACTTAAAAGCCATAGGT 67
```

RESULT 6
US-11-043-312-11
Sequence 11, Application US/11043312
; GENERAL INFORMATION:
; APPLICANT: COLOSI, PETER C.
; TITLE OF INVENTION: ACCESSORY FUNCTIONS FOR USE IN
;   RECOMBINANT AAV VIRION PRODUCTION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/043,312
; FILING DATE: 26-Jan-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/177,871
; FILING DATE: 19-Jun-2002
; APPLICATION NUMBER: US/08/745,957
; FILING DATE: 07-Nov-1996
; APPLICATION NUMBER: US 60/006,402
; FILING DATE: 09-Nov-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCRACKEN, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 0800-0007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3400
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-043-312-11

RESULT 7
US-10-707-003-1264
; Sequence 1264, Application US/1070/7003
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55030
; CURRENT APPLICATION NUMBER: US/10/707,003
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 46755
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 1264
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Human enterovirus C
US-10-707-003-1264

Query Match   18.9%; Score 18; DB 8; Length 95;
Best Local Similarity   69.2%; Pred. No. 1.1e+03;
Matches 18; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```
Qy    43 CACGCGAAAGGUCCCCGGUUCGAAAC 68
         ||| || |||||| |  ||| ||||
Db     8 CACGCGUGAGCUCCGGCGUUCGAAGC 33
```

RESULT 8
US-10-604-984-1264
; Sequence 1264, Application US/10604984
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY
; FILE REFERENCE: 55010
; CURRENT APPLICATION NUMBER: US/10/604,984
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 46755
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 1264
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Human enterovirus C
US-10-604-984-1264

Query Match   18.9%; Score 18; DB 6; Length 117;
Best Local Similarity   39.2%; Pred. No. 1.1e+03;
Matches 29; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

```
Qy    16 AGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAACACCGGGCGG 75
         ||:||:| :: ..:|: ...||| ::|.....|||||...|||||  |||
Db     7 AGUGUAAUAAUUUAGAAUUUCACCCAACAUGGUGUGACUCGUUUGUUCAGAAGCAGG 66
```

RESULT 9
US-10-153-469A-3
; Sequence 3, Application US/10153469A
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOT A.
; APPLICANT: BUECHTER, DOUGLAS
; BROKAW, JANE
; ZHANG, GUANGHUI
; PAOLELLA, DAVID
; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DILWORTH & BARRESE
; STREET: 333 EARLE OVINGTON BOULEVARD
; CITY: UNIONDALE
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 11553
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/153,469A
; FILING DATE: 22-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,768
; FILING DATE: 09-OCT-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: STEEN, JEFFREY S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 228-8484
; TELEFAX: (516) 228-8516
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-153-469A-3

Query Match   18.7%; Score 17.8; DB 6; Length 100;
Best Local Similarity   72.4%; Pred. No. 1.3e+03;
Matches 21; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

```
Qy    45 CGCGAAAGGUCCCCGGUUCGAAACCGGGC 73
         |||||||||| ||  || ||||| || |||
Db    48 CCCGAAAGGTCCGCGGTGGCGATAGCGGC 76
```

RESULT 10
US-10-932-182A-173417/c
; Sequence 173417, Application US/10932182A
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
;
; SEQ ID NO 173417
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-173417

```
Qy    15 UAGUGUAGUGGUUAUCACGUUCGCCUAACACG 46
         ||:||:||| : |::|||| |::| |||||||
Db    88 TAGTGTAGTGGTTATCATCCCACCCTTCCAAG 57
```

RESULT 11
US-10-605-923-13759/c
; Sequence 13759, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 13759
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-13759

Query Match   18.5%; Score 17.6; DB 6; Length 96;
Best Local Similarity   46.9%;
Matches   15; Conservative   8; Mismatches   9; Indels   0; Gaps   0;

```
Qy    20 UAGUGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGGGUUCGGAAAACCGGGGGGAAAC 79
         ||:|||:||||||||||||| ||| ||||||| || |:|||| |||||||:|||||||||||
Db   102 TATAGGTTTTCCAGTATGCTTATGTGTGACTTTGACTCAATTCCAAACTTGATTAAAAT 43
```

RESULT 12
US-10-605-924-9585/c
; Sequence 9585, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55004
; CURRENT APPLICATION NUMBER: US/10/605,924
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 9585
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-924-9585

Query Match   18.5%; Score 17.6; DB 7; Length 104;
Best Local Similarity   42.2%;
Matches   27; Conservative   8; Mismatches   29; Indels   0; Gaps   0;

```
Qy    80 AAAG 83
         ||||
Db    42 AAAG 39
```

RESULT 13
US-11-021-016-12

```
Qy    80 AAAG 83
         ||||
Db    42 AAAG 39
```

; Sequence 12, Application US/11021016
; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: IMPROVED POLYMERASE III-BASED EXPRESSION OF THERAPEUTIC
; TITLE OF INVENTION: RNAS
; CURRENT APPLICATION NUMBER: US/11/021,016
; CURRENT FILING DATE: 2004-12-23
; FILE REFERENCE: MBH00-919-E
; PRIOR APPLICATION NUMBER: 09/630,846
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 08/512,861
; PRIOR FILING DATE: 1995-08-07
; PRIOR APPLICATION NUMBER: 08/293,520
; PRIOR FILING DATE: 1994-08-19
; PRIOR APPLICATION NUMBER: 08/337,608
; PRIOR FILING DATE: 1994-11-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 112
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TR2-B tRNA
; OTHER INFORMATION: Chimera.
US-11-021-016-12

Query Match   18.5%; Score 17.6; DB 8; Length 112;
Best Local Similarity   54.7%;
Matches   35; Conservative   0; Mismatches   29; Indels   0; Gaps   0;

```
Qy    28 AUCACGUUCGCCUAACACGCGGAAAGGUCCCCGGGUUCGGAAAACCGGGGGGAAACCAAAGACAG 87
         ||||||| |||| ||:||  ||||:||||||||||||||:||||||| |||||:|| ||||||||
Db    28 AGCGUGCUGGGCCCARAACCCAGAGAGUCGAUGAGUGGAACACUGCGCCACUCAAAAAAAG 87
```

RESULT 14
US-10-605-923-17798/c
; Sequence 17798, Application US/10605923
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AN
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 55000
; CURRENT APPLICATION NUMBER: US/10/605,923
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 1515668
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 17798
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-605-923-17798

Query Match   18.3%; Score 17.4; DB 7; Length 66;
Best Local Similarity   47.5%;
Matches   28; Conservative   5; Mismatches   26; Indels   0; Gaps   0;

```
Qy    88 UCGC 91
         ||||
Db    88 CCGC 91
```

```
Qy    12 CCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGGGUUCGGAAAACCG 70
         |||||  |||||||||||||| |||||||||||| ||||:||||||||| |||||  || |||
Db    65 CTGACGTGGAACCATCACCCGGAACCATCACCCGGAACCCAGAGAGGCGGGAGGGTCGGTGATGTGGAACCG 7
```

RESULT 15
US-10-605-924-12307/c
; Sequence 12307, Application US/10605924
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY GENES AN

```
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: 55004
;   CURRENT APPLICATION NUMBER: US/10/605,924
;   CURRENT FILING DATE:  2003-11-06
;   NUMBER OF SEQ ID NOS: 1388402
;   SOFTWARE: Patentin version 3.2
;
;   SEQ ID NO 12307
;   LENGTH: 66
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;
US-10-605-924-12307

Query Match     18.3%;  Score 17.4;  DB 7;  Length 66;
Best Local Similarity   47.5%;  Pred. No. 1.6e+03;
Matches   28;  Conservative   5;  Mismatches   26;  Indels   0;  Gaps   0;

Qy       12 CCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCCGAAAAGGUUCCCGGUUCGAAAACCG 70
               | ||| | | :| | | | : ||||||| :| | |  |:|  : |:| |:| |||||
Db       65 CTGACGTCGGACCATCATCACCCGAACCCACAGAGGCGGAGGGTCGGGTGATGTGGAACCG  7
```

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: February 18, 2005, 21:00:02 ; Search time 1819 Seconds
(without alignments)
1987.963 Million cell updates/sec

Title: US-10-820-820-4
Perfect score: 95
Sequence: 1 acccguuguuccguaguguu..........aaacaaagacacagucgcuuu 95

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 2048674

Minimum DB seq length: 0
Maximum DB seq length: 150

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40.4	42.5	57	2	BF031637	BF031637 601558122
2	31	32.6	150	5	BU275850	BU275850
3	30.2	31.8	71	9	BX203515	BX203515 Danio rer
4	30	31.6	135	6	CB495943	CB495943 Cr_Emb_08
5	29.2	30.7	130	4	BI845249	BI845249 omykgroo0
6	29.2	30.7	147	6	AL763279	AL763279 fs92a07.y
7	28.2	29.7	124	9	DR36G28	DR36G28 Arabidops
8	26.6	28.0	136	8	AZ927512	AZ927512
9	26.4	27.8	137	8	BZ396589	BZ396589
10	26.4	27.8	144	9	AL985516	AL985516 Danio rer
11	25.8	27.2	149	6	BX166029	BX166029 Danio rer
12	25.6	26.9	126	7	AL736659	AL736659 Danio rer
13	25.6	26.9	126	9	H04713	H04713 e17-1.3.-3
14	25.2	26.5	109	6	CD768762	CD768762 AGENCOURT
15	25.2	26.5	112	6	CD769207	CD769207 AGENCOURT
16	24.8	26.1	37	9	AL757571	AL757571 Arabidops
17	24.8	26.1	134	9	BX126117	BX126117 Danio rer
18	24.6	25.9	122	5	BQ209653	BQ209653 UI-R-EP0-
19	24.4	25.7	121	1	AI013006	AI013006 EST207457
20	24.2	25.5	64	2	BF118530	BF118530 SWOvl3CAN
21	24.2	25.5	126	8	BX247709	BX247709 Danio rer
22	24	25.3	103	1	AU259857	AU259857
23	24	25.3	120	9	BX233421	BX233421 Danio rer
c 24	24	25.3	122	9	AL758258	AL758258 Arabidops
c 24	24	25.3	123	9	BX148475	BX148475 Danio rer
c 25	23.8	25.1	124	5	BW501761	BW501761
c 26	23.8	25.1	128	8	BH415441	BH415441
c 27	23.8	25.1	111	7	CK129105	CK129105
c 28	23.6	24.8	112	4	BI301836	BI301836
c 29	23.6	24.8	113	9	CD769729	CD769729
c 30	23.6	24.8	140	5	BQ481087	BQ481087
c 31	23.6	24.8	143	4	BI302103	BI302103
c 32	23.6	24.8	149	2	AW144501	AW144501
c 33	23.4	24.6	150	7	CV251165	CV251165
c 34	23.4	24.6	123	4	BM114423	BM114423
c 35	23.2	24.4	106	7	AW834645	AW834645
c 36	23.2	24.4	124	5	BQ342244	BQ342244
c 37	23.2	24.4	129	8	BZ619297	BZ619297
c 38	23.2	24.4	150	8	BZ619296	BZ619296
c 39	23	24.2	138	7	CO739722	CO739722
c 40	23	24.2	143	7	CO739864	CO739864
c 41	23	24.2	146	7	CO700047	CO700047
c 42	23	24.0	150	7	CO739938	CO739938
c 43	22.8	24.0	137	8	BI841646	BI841646
c 44	22.6	23.8	73	9	AL768946	AL768946
c 45	22.6	23.8	121	9	CG823338	CG823338 SOYATI4TH

ALIGNMENTS

RESULT 1
BF031637
LOCUS   BF031637   57 bp   mRNA   linear   EST 10-OCT-2000
DEFINITION 601558122F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827860 5',
            mRNA sequence.
ACCESSION   BF031637
VERSION   BF031637.1 GI:10739349
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 57)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM497 row: l column: 05
            High quality sequence stop: 57.
FEATURES   Location/Qualifiers
     source   1..57
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3827860"
                     /tissue_type="hypernephroma"
                     /clone_lib="NIH_MGC_58"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattaggcc);
                     Double-stranded cDNA was prepared from cell line RNA. 5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence: 5'-CACGCGCCATTATGGCC-3' and 3' adaptor
                     sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACGCGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C, G, or T).
                     Insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
                     contained inserts and was constructed by Clontech
                     full-length clones (Palo Alto, CA)."

ORIGIN

Qy   18 UGUAGUGGGUUAUCACGUUCGGCCUAACACGCGAAAGGUCCCCGGUUCGAA 67
         :|:||||||||||||||:|||||||||||||||||:|||||:|||||:||
Db   1 TGTAGCGGTTATCACATTCGGCCTCACACGCGAAAGGTCCCCGGTTTATPA 50

RESULT 2

LOCUS   BU275850   150 bp   mRNA   linear   EST 03-JAN-2003
DEFINITION Cr_Emb_08F08_TEXP1 Convoluta roscoffensis embryos from Eva Jiménez
            Symsagittifera roscoffensis cDNA clone Cr_Emb_08F08 5', mRNA
            sequence.
ACCESSION   BU275850
VERSION   BU275850.1 GI:27476620
KEYWORDS   EST.
SOURCE   Symsagittifera roscoffensis
  ORGANISM Symsagittifera roscoffensis
            Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Acoelomorpha;
            Acoela; Sagittiferidae; Symsagittifera.
REFERENCE   1 (bases 1 to 150)
  AUTHORS   Blaxter,M.L., Jiménez,E., Rosie,A., Aboobaker,A. and Salo,E.
  TITLE   A survey of genes expressed in the acoel flatworm Convoluta
            roscoffensis
  JOURNAL   Unpublished (2002)
COMMENT   Contact: Blaxter ML
            Institute of Cell, Animal and Population Biology
            University of Edinburgh
            Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
            3JT, UK.
            Tel: +44 131 650 6760
            Fax: +44 131 670 5450
            Email: mark.blaxter@ed.ac.uk
            The library was prepared by Eva Jiménez, University of Barcelona,
            Spain The sequencing was performed by Eva Jiménez, Aziz Aboobaker
            and Aiile Rosie Edinburgh Phylogenomics Programme, ICAPB,
            Edinburgh, UK.The sequence contained a polyA tail (trimmed)
            PCR Primers
            FORWARD: T7PL
            BACKWARD: triple 5 Exseq
            Plate: 08 row: F column: 08
            Seq primer: TEXP1
            High quality sequence stop: 150.
FEATURES   Location/Qualifiers
     source   1..150
                     /organism="Symsagittifera roscoffensis"
                     /mol_type="mRNA"
                     /db_xref="taxon:84072"
                     /clone="Cr_Emb_08F08"
                     /sex="mixed"
                     /dev_stage="embryo"
                     /clone_lib="Convoluta roscoffensis embryos from Eva
                     Jiménez"
                     /note="Vector: lambda triplex; Site 1: EcoRI; Site 2:
                     HindIII; The library was prepared by Eva Jiménez,
                     University of Barcelona, Spain The sequencing was
                     performed by Eva Jiménez, Aziz Aboobaker and Aiile Rosie,
                     Edinburgh Phylogenomics Programme, ICAPB, Edinburgh, UK."
ORIGIN

Query Match   32.6%; Score 31; DB 5; Length 150;
Best Local Similarity 44.8%; Pred. No. 1.1;
Matches 39; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

Qy   7 GGUUCCGUAGUGUGUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAA 66
         ||::||| |:| ||||| |||:||||||||||||||||||||||||||||||
Db   26 GGGAGCAGTGGTGGTGAAGTGGTTAAGGTCTCCGCTCTCAATCGAAAGGTCGGGATGTTCGGAG 85

ORIGIN

Query Match   42.5%; Score 40.4; DB 2; Length 57;
Best Local Similarity 66.0%; Pred. No. 0.00026;
Matches 33; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy   7 GGUUCCGUAGUGUGUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAA 66
         ||::|||:||| |:| ||||| |||:|||||||||||||||||||||||||
Db   26 GGGAGCAGTGGTGAAGTGGTTAAGGTCTCCGCTCTCAATCGAAAGGTCGGGATGTTCGGAG 93

Db   86 GCCCACCATGATCCGTGCTCGGTTGCTT 112
         ||:|||||||| | |||| |:||:||

Db

RESULT 3

LOCUS   BX203515   71 bp   DNA   linear   GSS 13-MAR-2003
DEFINITION Danio rerio genomic clone DKEY-224D6, genomic survey sequence.
ACCESSION   BX203515
VERSION   BX203515.1 GI:28035401
KEYWORDS   GSS.
SOURCE   Danio rerio (zebrafish)
  ORGANISM Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 71)
  AUTHORS   Humphray,S.J., Huckle,E. and Durham,J.L.
  TITLE   Direct Submission
  JOURNAL   Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Unpublished
COMMENT   This sequence was generated from the T7 end of BAC 224D6 is
            part of the DanioKey BAC library created by R. Plasterk and N.V.
            Keygene. Further details:
            http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES   Location/Qualifiers
     source   1..71
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-224D6"
                     /clone_lib="DKEY-224D6"
                     /note="vector pindigoBAC-536"
ORIGIN

Query Match   31.8%; Score 30.2; DB 9; Length 71;
Best Local Similarity 49.3%; Pred. No. 1.9;
Matches 33; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

Qy   9 UUUCCGUAGUGUGUGUGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAAC 68
         |:|:|| || || || || ||:|||:|| || ||||||| ||| ||:||:|| |||:
Db   2 TTGGAGTGGCTCAGTGGTTAGTACCGTCGCCTCACAGTAAAAAGGTCACTGGTTYAAATC 61

Qy   69 CGGGCGG 75
         ||||| |
Db   62 CCGGCTG 68

RESULT 4

LOCUS   CB495943   135 bp   mRNA   linear   EST 27-MAR-2003
DEFINITION omykgroo003031 Oncorhynchus mykiss Chilliwack River steelhead whole
            Oncorhynchus mykiss cDNA, mRNA sequence.
ACCESSION   CB495943
VERSION   CB495943.1 GI:29307169
KEYWORDS   EST.
SOURCE   Oncorhynchus mykiss (rainbow trout)
  ORGANISM Oncorhynchus mykiss
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE   1 (bases 1 to 135)
  AUTHORS   GRASP Consortium, Davidson,W.S., Koop,B.F. and
            http://web.uvic.ca/cbr/grasp.
  TITLE   A survey of Salmo salar transcripts from high complexity cDNA
            libraries
  JOURNAL   Unpublished (2002)
COMMENT   Contact: Koop BF
            Centre for Biomedical Research
            University of Victoria
            PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
            Tel.: 250 472 4067

FEATURES
  source
    1..135
    /organism="Oncorhynchus mykiss"
    /mol_type="mRNA"
    /strain="Chilliwack River steelhead"
    /db_xref="taxon:8022"
    /clone_lib="Oncorhynchus mykiss Chilliwack River steelhead
    whole"
    /note="Vector: pBluescriptISK+; Library Creator: Matthew
    L. Rise, BF Koop ; Rainbow trout tissue contributors:
    Robert Devlin (DFO, Vancouver, B.C.)"
ORIGIN

Query Match   31.6%;   Score 30;   DB 6;   Length 135;
Best Local Similarity   48.6%;   Pred. No. 2.5;
Matches 34;   Conservative 11;   Mismatches 25;   Indels 0;   Gaps 0;

Qy   14 GUAGUGUAGUGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGGAAACCGGGC 73
        :|||: : ||||| :: ||||: ||||||: ||:: ||||: ||
Db   65 GUAGCCUPAGUGGUTUAGAGCGTTGGACTAGTAGTACCGGAAGAAGGTTGGCGAGTTCAAAACCCCCA 124

Qy   74 GGAAACAAAG 83
        |||||||
Db   125 GCTGACAAGG 134

RESULT 5
LOCUS   BI845249   130 bp   mRNA   linear   EST 04-OCT-2001
DEFINITION   fs92a07.y1 Zebrafish neuronal Danio rerio cDNA clone IMAGE:5077140
          5', mRNA sequence.
ACCESSION   BI845249
VERSION   BI845249.1   GI:15957772
KEYWORDS   EST.
SOURCE   Danio rerio (zebrafish)
  ORGANISM   Danio rerio
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
          Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 130)
AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
          Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
          Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
          Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
          Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
          Waterston,R. and Wilson,R.
TITLE   WashU Zebrafish EST Project 1998
JOURNAL   Unpublished (1998)
COMMENT   Contact: Stephen L. Johnson
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: zbrafish@watson.wustl.edu
          cDNA Library constructed by S. Lin DNA Sequencing by: Washington
          University Genome Sequencing Center Clone distribution: the
          I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
          Seq primer: T3 ET from Amersham.
FEATURES
  source   1..130
          /organism="Danio rerio"
          /mol_type="mRNA"
          /db_xref="taxon:7955"
          /clone="IMAGE:5077140"
          /sex="mixed"
          /dev_stage="adult"
          /lab_host="DH10B (phage-resistant)"

Fax: 250 472 4075
Email: bkoop@uvic.ca
Centre for Biomedical Research, University of Victoria cDNA
preparation and sequencing: Roberto Alberto, Marianne
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop,
bioinformatics: Gordon D Brown.

ORIGIN

Query Match   30.7%;   Score 29.2;   DB 4;   Length 130;
Best Local Similarity   53.4%;   Pred. No. 5;
Matches 31;   Conservative 9;   Mismatches 18;   Indels 0;   Gaps 0;

Qy   8 GUUUCCGUAGUGUAGUGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGA 65
      |: |:: |||: ||| : ||||| : ||||: || ||||| : ||||||
Db   63 GTCACGGTTGCGCGCGAGTTGGGTTAGCACGGATCCCCTCACAGCAAGAAGAGATCACTGGGTTCGA 6

RESULT 6
LOCUS   AL763279   147 bp   DNA   linear   GSS 01-APR-2004
DEFINITION   Arabidopsis thaliana T-DNA flanking sequence GK-035E01-015008,
          genomic survey sequence.
ACCESSION   AL763279
VERSION   AL763279.1   GI:21512136
KEYWORDS   GSS.
SOURCE   Arabidopsis thaliana (thale cress)
  ORGANISM   Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
AUTHORS   Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE   GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
          the identification of T-DNA insertion mutants in Arabidopsis
          thaliana
JOURNAL   Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE   22755829
PUBMED   12874060
REFERENCE   2
AUTHORS   Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
          Weisshaar,B.
TITLE   An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
          flanking sequence tag-based reverse genetics
JOURNAL   Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE   23117147
PUBMED   14756321
REFERENCE   3
AUTHORS   Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
          Weisshaar,B.
TITLE   High-throughput generation of sequence indexes from T-DNA
          mutagenized Arabidopsis thaliana lines
JOURNAL   BioTechniques 35 (6), 1164-1168 (2003)
PUBMED   14682050
REFERENCE   4 (bases 1 to 147)
AUTHORS   Rosso,M.G., Li,Y., Strizhov,N. and Weisshaar,B.
TITLE   Direct Submission
JOURNAL   Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
          Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT   This sequence has been recovered from the left border of the T-DNA.
          It indicates an insertion close to or within gene At3g05830.
          Details on the protocols used for generation of the sequence are
          described in References 1-3. The sequences are generated at the MPI
          for Plant Breeding Research in the context of the GABI-Kat project.
          GABI-Kat is part of the German Plant Genomics program designated
          'GABI'. Information on line availability can be found at:
          http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
  source   1..147
          /organism="Arabidopsis thaliana"
          /mol_type="genomic DNA"
          /strain="Columbia 0"
          /db_xref="taxon:3702"
          /clone="GK-035E01-015008"
          /clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/clone_lib="zebrafish neuronal"
/note="Organ: brain; Vector: pBluescript (modified);
Site_1: DraIII(Y); Site_2: DraIII(X); Library is cloned
directionally between the DraIII(X) and DraIII(Y) sites
and has been amplified. Library constructed by S. Lin."

ORIGIN
```
              /ecotype="Col-0"
              /note="PCR was performed on DNA from Arabidopsis thaliana
              plants (T1) which were transformed with the T-DNA from
              vector pAC161 (GenBank accession number: AJ537514). The
              lines contain one or more T-DNA insertions. The DNA
              fragment(s) resulting from the PCR were directly sequenced
              to determine the genomic sequence flanking the insertion.
              T-DNA derived sequences were removed."

Qy   23 UGGUUAUCACGUUCGCCUAACACGGCGAAAGGUCCCCGGGUUCGAAAACCGGGGCGGGGAAACA 80
        ||:::||  |||||||||||||||||||||||  |||||||| ||:|||||||||||||||||
Db   94 TGGTTAGACCGTTCGTTCTTTATGAGCCGAAGGTCGCGGGTTCGAGCCCCCGCCGGGGAAGCA 37
```

RESULT 7
DR36G28/c
```
LOCUS       DR36G28                  124 bp    DNA     linear   GSS 22-NOV-2002
DEFINITION  Danio rerio genomic clone DKEY-36G2, genomic survey sequence.
ACCESSION   AL985516
VERSION     AL985516.1  GI:25180237
KEYWORDS    GSS.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 124)
  AUTHORS   Humphray,S.J., Huckle,E. and Hunt,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
            Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk Unpublished
COMMENT     This sequence was generated from the SP6 end of BAC 36G2. 36G2 is
            part of the DanioKey BAC Library created by R. Plasterk and N.V.
            Keygene.
            Further details: http://www.sanger.ac.uk/projects/D_rerio/.
FEATURES             Location/Qualifiers
     source          1..124
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-36G2"
                     /tissue_type="Testis"
                     /notes="vector pindigoBAC-536"
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ORIGIN
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Query Match             29.7%;  Score 28.2;  DB 9;  Length 124;
  Best Local Similarity   49.3%;  Pred. No.12;
  Matches   36;  Conservative    9;  Mismatches   28;  Indels    0;  Gaps    0;

Qy    8 GUUUCCGUAGUGUGUGUUAUCACGUUCGCCUAACACGGCGAAAGGUCCCCGGGUUCGAAA 67
        |||||||   ||||||||||
Db   97 GTCACAATGGCTCAGTGGGTAGCATGGATCGGCCCTCACACAACAAGAGAGGTCACTGGGTTTTGAGC 38

Qy   68 CCGGGGCGGGGAAACA 80
        || ||||
Db   37 CCTGGGCTGGGTCA 25
```

RESULT 8
A2927512/c
```
LOCUS       A2927512                 136 bp    DNA     linear   GSS 01-APR-2001
DEFINITION  476.d1t25f11.s1 Saccharomyces castellii NRRL Y-12630 Naumovia
            castellii genomic clone 476.d1t25f11.s1, genomic survey sequence.
ACCESSION   A2927512
VERSION     A2927512.1  GI:13498416
KEYWORDS    GSS.
SOURCE      Naumovia castellii
  ORGANISM  Naumovia castellii
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Naumovia.
REFERENCE   1  (bases 1 to 136)
  AUTHORS   Cliften,P.F., Hillier,L.W., Fulton,L., Graves,T., Miner,T.,
            Gish,W.R., Waterston,R.H. and Johnston,M.
  TITLE     Surveying Saccharomyces genomes to identify functional elements by
            comparative DNA sequence analysis
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Johnston M
            Department of Genetics
            Washington University Medical School
            Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
            Tel: 314 362 2735
            Fax: 314 362 7855
            Email: mj@genetics.wustl.edu
            Class: random plasmid subclone.
FEATURES             Location/Qualifiers
     source          1..136
                     /organism="Naumovia castellii"
                     /mol_type="genomic DNA"
                     /strain="NRRL Y-12630 (CBS 4309)"
                     /db_xref="taxon:27288"
                     /clone="476.d1t25f11.s1"
                     /clone_lib="Saccharomyces castellii NRRL Y-12630"
                     /note="Random genomic sequence "
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ORIGIN
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Query Match             28.0%;  Score 26.6;  DB 8;  Length 136;
  Best Local Similarity   68.3%;  Pred. No.49;
  Matches   28;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy   40 UAACACGGCGAAAGGUCCCCGGGUUCGAAAACCGGGGCGGGGAAACA 80
        :|||||||||| |||| |:|||| ||:|||| |||||||||||| ||
Db  135 TAACACGCCAGAACCGTCCCCAGTTCGATCCTGGGGCGGGGAAAATCA 95
```

RESULT 9
BZ396589
```
LOCUS       BZ396589                 137 bp    DNA     linear   GSS 30-APR-2003
DEFINITION  EINAN55TF EI_10_12_KB Entamoeba invadens genomic clone EINAN55,
            genomic survey sequence.
ACCESSION   BZ396589
VERSION     BZ396589.1  GI:30243136
KEYWORDS    GSS.
SOURCE      Entamoeba invadens
  ORGANISM  Entamoeba invadens
            Eukaryota; Entamoebidae; Entamoeba.
REFERENCE   1  (bases 1 to 137)
  AUTHORS   Wang,Z., Samuelson,J., Clark,C.G., Eichinger,D., Paul,J., van
            Dellen,K., Hall,N., Anderson,I. and Loftus,B.
  TITLE     Gene discovery in the Entamoeba invadens genome
  JOURNAL   Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)
  MEDLINE   22684048
   PUBMED   12798503
COMMENT     Other_GSSs: EINAN55TR
            Contact: Brendan Loftus
            Department of Eukaryotic Genomics
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208
            Email: enta@igr.org
            DNA was provided by Daniel Eichinger
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1..137
                     /organism="Entamoeba invadens"
                     /mol_type="genomic DNA"
                     /strain="IP-1"
                     /db_xref="taxon:33085"
                     /clone="EINAN55"
```

ORIGIN

Qy   29 UCAGGUUCGCCUAACACGCGAAAAGGUCCCCGGGUUCGAAACCGG 80
         ||||| ||||||||:||:|||||||||||:|||:|||||||||||
Db   1 TCACATCAGTTTTACGTACTGAGGGTCCCCGGGTTCAATCCGGGCGGGAAACCA 52

RESULT 10
LOCUS   BX166029
DEFINITION   Danio rerio genomic clone DKEY-124P18, genomic survey sequence.
ACCESSION   BX166029
VERSION   BX166029.1 GI:27997576
KEYWORDS   GSS.
SOURCE   Danio rerio (zebrafish)
ORGANISM   Danio rerio
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
              Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 144)
AUTHORS   Humphray,S.J., Huckle,E. and Durham,J.L.
TITLE   Direct Submission
JOURNAL   Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
              Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
              humquery@sanger.ac.uk Unpublished
COMMENT   This sequence was generated from the T7 end of BAC 124P18. 124P18
              is part of the Daniokey BAC library created by R. Plasterk and N.V.
              Keygene. Further details:
              http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES   Location/Qualifiers
     source   1..144
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-124P18"
                     /tissue_type="Testis"
                     /note="vector pindigoBAC-536"

ORIGIN

Query Match   27.8%; Score 26.4; DB 8; Length 137;
Best Local Similarity   57.7%; Pred. No. 58;
Matches   30; Conservative   6; Mismatches 16; Indels   0; Gaps   0;

Qy   29 UCAGGUUCGCCUAACACGCGAAAAGGUCCCCGGGUUCGAAACCGGGCGGGAAACA 80
         |||| | | ||| ::| |||:|||:|:|||||||||||:|| || |||||||||||
Db   1 TCACATCAGTTTTACGTACTGAGGGTCCCCGGGTTCAATCCGGGCGGGAAACCA 52

ORIGIN

ORGANISM   Danio rerio
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
              Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 149)
AUTHORS   Humphray,S.J., Huckle,E. and Hunt,S.E.
TITLE   Direct Submission
JOURNAL   Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
              Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
              humquery@sanger.ac.uk Unpublished
COMMENT   This sequence was generated from the SP6 end of BAC 21E13. 21E13 is
              part of the Daniokey BAC library created by R. Plasterk and N.V.
              Keygene.
              Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES   Location/Qualifiers
     source   1..149
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-21E13"
                     /tissue_type="Testis"
                     /note="vector pindigoBAC-536"

Qy   28 AUCACGGUUCGCCUAACACGCGAAAAGGUCCCCGGGUUCGAAACCGGGCGGGAAACA 80
         |||| :|| ||||:||||| ||||:|||| :||||| |:|||||||||| ||||||||
Db   4 ATCACGATCACCTCACATCAAGAAGGTCGGTGGTTCGAGCCCCTGCTGTGGGATCA 56

RESULT 11
LOCUS   DR21E13S   149 bp   DNA   linear   GSS 27-NOV-2002
DEFINITION   Danio rerio genomic clone DKEY-21E13, genomic survey sequence.
ACCESSION   AL736659
VERSION   AL736659.1 GI:21348575
KEYWORDS   GSS.
SOURCE   Danio rerio (zebrafish)

ORIGIN

Query Match   48.5%; Score 26.4; DB 9; Length 144;
Best Local Similarity   48.5%; Pred. No. 59;
Matches   33; Conservative   9; Mismatches 26; Indels   0; Gaps   0;

Qy   12 CCGUAGUGUAGUGGUUAUCACGUUCGCCCUAACACGCGGAAAGGUCCCCGGUUCGAAACCGG 71
Db   21 CAGTTGTACAGTGGGTAGTACAATCGCCTCACAGCAAGAAGGTCGTAATGGTTCGATGATGG 80

Qy   72 GCCGAAAC 79
Db   81 GTTGCAGC 88

RESULT 12
LOCUS   H04713   126 bp   mRNA   linear   EST 20-JUN-1995
DEFINITION   Rattus norvegicus cDNA clone e17-1.3.3', mRNA sequence.
ACCESSION   H04713
VERSION   H04713.1 GI:867646
KEYWORDS   EST.
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
REFERENCE   1 (bases 1 to 126)
AUTHORS   Schwartz,P.E., Grieshaber,N.A., Grieshaber,S.S. and Majack,R.A.
TITLE   An expressed sequence tag from in vitro embryonic rat vascular
              smooth muscle cells
JOURNAL   Unpublished (1995)
COMMENT   Contact: Philip E. Schwartz
              Pediatrics and Cellular and Structural Biology
              University of Colorado Health Sciences Center
              4200 East Ninth Avenue, Denver, Colorado, 80262, USA
              Tel: (303) 270-4569
              Fax: (303) 270-8353
              Email: schwartz.p@defiance.hsc.colorado.edu.
FEATURES   Location/Qualifiers
     source   1..126
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="e17-1.3.3"
                     /clone_lib="Lambda Zap Express library of P. E. Schwartz
                     (9/93)"
                     /note="developmental-stage=Embryonic Day 17
                     Post-fertilization; tissue-type=Aorta; cell-type=Vascular
                     smooth muscle cell; sex=Male."

ORIGIN

Query Match   27.8%; Score 25.8; DB 9; Length 149;
Best Local Similarity   56.6%; Pred. No. 99;
Matches   30; Conservative   6; Mismatches 17; Indels   0; Gaps   0;

Qy   28 AUCACGGUUCGCCUAACACGCGAAAAGGUCCCCGGGUUCGAAACCGGGCGGGAAACA 80
         |||| :|| ||||:||||| ||||:|||| :||||| |:|||||||||| ||||||||
Db   4 ATCACGATCACCTCACATCAAGAAGGTCGGTGGTTCGAGCCCCTGCTGTGGGATCA 56

ORGANISM   Danio rerio
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
              Cypriniformes; Cyprinidae; Danio.

ORIGIN

Query Match   26.9%; Score 25.6; DB 7; Length 126;

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RESULT 13
Qy      CD768762
Matches Best Local Similarity 50.0%; Conservative 7; Pred. No. 1.1e+02;
        36; Conservative 7; Mismatches 29; Indels 0; Gaps 0;

Qy   15 UAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAAACCGGGCG 74
        |:||:|  ||||||  |||||| | ||||||||:| :| || ||||| ||:||||||||||
Db   51 TAGCTCAGTGGTAGAGCGCCCGCCTTGCCTAGGAAGGCGGCAAGGCCCCTGGGGTTCGGGTCGGTCCCCAGCT 110

Qy   75 GAAACAAGACA 86
        |||||||||||
Db  111 CTGAAAAAAGA 122
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```
RESULT 13
LOCUS        CD768762          109 bp    mRNA    linear    EST 02-JUL-2003
DEFINITION   AGENCOURT_14715419 NICHD_MM_Hyp1 Mus musculus cDNA clone
             IMAGE:6975107 5', mRNA sequence.
ACCESSION    CD768762
VERSION      CD768762.1  GI:32427264
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 109)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      Contact: Daniela S. Gerhard, Ph.D.
             Office of Cancer Genomics
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Pamela Mellon and Dr. Pat Chappell
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM3275 row: c  column: 10
             High quality sequence stop: 109.
FEATURES             Location/Qualifiers
     source          1..109
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6975107"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_MM_Hyp1"
                     /note="Organ: brain - normal mediobasal hypothalamus;
                     Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2:
                     SfiI (ggccgcctcggcc); Non-normalized full-length enriched
                     library 5' and 3' adapters were used in cloning as
                     follows: 5' adaptor sequence: 5'-CACGGCGCATTATGGCC-3' and
                     3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGCGGCCGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.08
                     kb (range .73-1.37 kb), 13/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech Laboratories (Palo Alto,
                     CA).Corp."
ORIGIN
```

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Qy      Best Local Similarity 26.5%; Score 25.2; DB 6; Length 109;
Matches Query Match 54.8%; Pred. No. 1.6e+02;
        34; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

Qy   25 GUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAAACCGGGCGGAAACAAAGA 84
        ||| | :||| |:||:| || |||||| || | ||||| ||:|||||| ||||||||||
Db   26 GGTAGAGCGCCTTGCCTAGGAAGGCGGCAAGGCCCCTGGGGTTCGGGTCGGTCCCCAGCTCTGAAAAAAAA 85

Qy   85 CA 86
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Db   85 CA 86
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```
RESULT 14
Db      CD769207                                                    86 AA 87
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```
RESULT 14
LOCUS        CD769207          112 bp    mRNA    linear    EST 02-JUL-2003
DEFINITION   AGENCOURT_14720166 NICHD_MM_Hyp1 Mus musculus cDNA clone
             IMAGE:6974510 5', mRNA sequence.
ACCESSION    CD769207
VERSION      CD769207.1  GI:32427709
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 112)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
COMMENT      Contact: Daniela S. Gerhard, Ph.D.
             Office of Cancer Genomics
             National Cancer Institute / NIH
             Bldg. 31 Rm10A07 Bethesda, MD 20892
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Pamela Mellon and Dr. Pat Chappell
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLCM3273 row: j  column: 13
             High quality sequence stop: 112.
FEATURES             Location/Qualifiers
     source          1..112
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6974510"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_MM_Hyp1"
                     /note="Organ: brain - normal mediobasal hypothalamus;
                     Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2:
                     SfiI (ggccgcctcggcc); Non-normalized full-length enriched
                     library 5' and 3' adapters were used in cloning as
                     follows: 5' adaptor sequence:
                     3' adaptor sequence: 5'-CACGGCGCATTATGGCC-3' and
                     5'-ATTCTAGAGGCCGAGCGGCCGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.08
                     kb (range .73-1.37 kb), 13/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech Laboratories (Palo Alto,
                     CA).Corp."
ORIGIN
```

```
Qy      Best Local Similarity 26.5%; Score 25.2; DB 6; Length 112;
Matches Query Match 54.8%; Pred. No. 1.6e+02;
        34; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

Qy   25 GUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAAACCGGGCGGAAACAAAGA 84
        ||| | :||| |:||:| || |||||| || | ||||| ||:|||||| ||||||||||
Db   26 GGTAGAGCGCCTTGCCTAGGAAGGCGGCAAGGCCCCTGGGGTTCGGGTCGGTCCCCAGCTCTGAAAAAAAA 85

Qy   85 CA 86
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Db   86 AA 87
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```
RESULT 15
LOCUS        AL757571          37 bp    DNA    linear    GSS 01-APR-2004
DEFINITION   Arabidopsis thaliana T-DNA flanking sequence GK-150B02-013073,
```

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ACCESSION   AL757571
VERSION     AL757571.1  GI:21495919
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana
  ORGANISM  Arabidopsis thaliana (thale cress)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
  TITLE     GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
  JOURNAL   Bioinformatics 19 (11), 1441-1442 (2003)
   MEDLINE  22755829
   PUBMED   12874060
REFERENCE   2
  AUTHORS   Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
            Weisshaar,B.
  TITLE     An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
            flanking sequence tag-based reverse genetics
  JOURNAL   Plant Mol. Biol. 53 (1-2), 247-259 (2003)
   MEDLINE  23117147
   PUBMED   14756321
REFERENCE   3
  AUTHORS   Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
            Weisshaar,B.
  TITLE     High-throughput generation of sequence indexes from T-DNA
            mutagenized Arabidopsis thaliana lines
  JOURNAL   BioTechniques 35 (6), 1164-1168 (2003)
   PUBMED   14682050
REFERENCE   4   (bases 1 to 37)
  AUTHORS   Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence has been recovered from the left border of the T-DNA.
            It indicates an insertion close to or within gene At3g50840.
            Details on the protocols used for generation of the sequence are
            described in References 1-3. The sequences are generated at the MPI
            for Plant Breeding Research in the context of the GABI-Kat project.
            GABI-Kat is part of the German Plant Genomics program designated
            'GABI'. Information on line availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1..37
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-150E02-013073"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /ecotype="Col-0"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161 (GenBank accession number: AJ537514). The
                     lines contain one or more T-DNA insertions. The DNA
                     fragment(s) resulting from the PCR were directly sequenced
                     to determine the genomic sequence flanking the insertion.
                     T-DNA derived sequences were removed."
ORIGIN

Qy          28 AUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUC 63
               |:|||||:||  |||||:|||||||||||||||||| :|
Db           2 AUCACGUUUGCCUPACACGCAAAAGGCCUCGGGAUC 37

Query Match    26.1%;  Score 24.8;  DB 9;  Length 37;
Best Local Similarity    66.7%;
Matches    24;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;
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Search completed: February 18, 2005, 22:33:08

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: February 18, 2005, 22:02:48 ; Search time 313 Seconds
           (without alignments)
           1799.921 Million cell updates/sec

Title: US-10-820-820-4
Perfect score: 95
Sequence: 1 accguuggguuccguaguguu.............aaacaaagacacagucgcuuuu 95

Scoring table: IDENTITY.NUC
                Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs, 295248155 residues

Total number of hits satisfying chosen parameters: 5307602

Post-processing: Minimum Match 0%
Minimum DB seq length: 0
Maximum DB seq length: 150

Maximum Match 100%
Listing first 45 summaries

Database :   Published_Applications_NA.*
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2:  /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3:  /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
4:  /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	100.0	100.0	95	16	US-10-361-028-8	Sequence 8, Appli
2	95	100.0	18	18	US-10-820-820-4	Sequence 4, Appli
3	74.8	78.7	88	10	US-09-974-974-5	Sequence 5, Appli
4	74.8	78.7	88	10	US-10-475-851A-3	Sequence 3, Appli
5	74.8	78.7	138	10	US-09-974-974-17	Sequence 17, Appli
6	74.8	78.7	141	16	US-10-361-028-52	Sequence 52, Appli
7	74.8	78.7	142	16	US-10-361-028-49	Sequence 49, Appl
8	74.8	78.7	142	16	US-10-361-028-50	Sequence 50, Appl
9	74.8	78.7	142	16	US-10-361-028-51	Sequence 51, Appl
10	74.8	78.7	142	16	US-10-361-028-53	Sequence 53, Appl
11	74	77.9	128	18	US-10-820-820-3	Sequence 3, Appli

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

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12  73  76.8  18  US-10-820-820-1     Sequence 1, Appli
13  73  76.8  18  US-10-820-820-2     Sequence 2, Appli
14  69.8 73.5 18  US-10-820-820-5     Sequence 5, Appli
15  66.8 70.3 18  US-10-820-820-7     Sequence 7, Appli
16  66  69.5  18  US-10-820-820-6     Sequence 6, Appli
17  63  66.3  18  US-10-738-642-57    Sequence 57, Appl
18  35.2 37.1 19  US-10-857-625-384   Sequence 384, App
19  35.2 37.1 19  US-10-857-625-404   Sequence 404, App
20  35.2 37.1 19  US-10-857-625-407   Sequence 407, App
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22  27  28.4  18  US-10-807-755-25    Sequence 25, Appl
23  26  27.4  18  US-10-067-956-3     Sequence 3, Appli
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25  26  27.4  18  US-10-898-106-4     Sequence 4, Appli
26  26  27.4  18  US-10-898-106-3     Sequence 3, Appli
27  26  27.4  17  US-10-057-783A-30   Sequence 30, Appl
28  26  27.4  17  US-10-057-783A-27   Sequence 27, Appl
29  26  27.4  14  US-10-083-357-557   Sequence 557, App
30  25.8 27.2 14  US-10-083-357-348   Sequence 348, App
31  25.4 26.7 132 US-10-083-357-348   Sequence 348, App
32  25.2 26.5 64  US-09-974-300-8411  Sequence 8411, Ap
33  25.2 26.5 64  US-09-974-300-8428  Sequence 8428, Ap
34  25.2 26.5 64  US-09-974-300-8437  Sequence 8437, Ap
35  25  26.3  9   US-09-974-300-8437  Sequence 8437, Ap
36  25  26.3  9   US-09-974-300-4366  Sequence 4366, Ap
37  25  26.3  9   US-09-974-300-4385  Sequence 4385, Ap
38  25  26.3  9   US-09-974-300-4400  Sequence 4400, Ap
39  25  26.3  9   US-09-974-300-4442  Sequence 4442, Ap
40  25  26.3  9   US-09-974-300-8401  Sequence 8401, Ap
41  25  26.3  9   US-09-974-300-8420  Sequence 8420, Ap
42  25  26.3  9   US-09-974-300-8425  Sequence 8425, Ap
43  25  26.3  9   US-09-974-300-8435  Sequence 8435, Ap
44  25  26.3  18  US-10-820-820-13    Sequence 13, Appl
45  24.4 25.7 17  US-10-282-1222A-27179 Sequence 27179, A
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RESULT 1
US-10-361-028-8

; Sequence 8, Application US/10361028
; Publication No. US2003019471A1
GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361,028
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US/09/704,525
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US/10/361,028
; PRIOR APPLICATION NUMBER: JP 316133/1999
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 95
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
; OTHER INFORMATION: sequence of the transcript of the human placental tRNAVal
US-10-361-028-8

Query Match   100.0%; Score 95; DB 16; Length 95;
Best Local Similarity   100.0%;
Matches   95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCGUUGGGUUCCGUAGUGUUAGUGGGUUAUCACGUUCGCCUUAACACGCGAAAGGUCCCGG 60
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Db   1 ACCGUUGGUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGCGCGGAAACAAAGACAGUCGCUUU 95
       |||||||||||||||||||||||||||||||||||
Db 61 UUCGAAACCGGGCGCGGAAACAAAGACAGUCGCUUU 95

RESULT 2
US-10-820-820-4
; Sequence 4, Application US/10820820
; Publication No. US20040198689A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0055-00000
; CURRENT APPLICATION NUMBER: US/10/820,820
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US/08/763,590
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 95
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; SEQ ID NO 4
; OTHER INFORMATION: sequence of the transcript of human placental tRNA Val
US-10-820-820-4

Query Match   100.0%; Score 95; DB 18; Length 95;
Best Local Similarity   100.0%; Pred. No. 4.7e-26;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGCGCGGAAACAAAGACAGUCGCUUU 95
       ||||||||||||||||||||||||||||||||||||
Db 61 UUCGAAACCGGGCGCGGAAACAAAGACAGUCGCUUU 95

RESULT 3
US-09-974-974-5
; Sequence 5, Application US/09974974
; Publication No. US20030013095A1
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; APPLICANT: Tomoko WARASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; TITLE OF INVENTION: target RNA by recognizing another molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,974
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNAVal promoter sequence

US-09-974-974-5

Query Match   78.7%; Score 74.8; DB 10; Length 88;
Best Local Similarity   91.9%; Pred. No. 2.3e-18;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60
       |||||||||| |||||||| |||||||||||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGCGCGGAAACAAAGACA 86
       |||||||||||||||| | ||||||||
Db 61 UUCGAAACCGGGCGCGGCACUACAAAAACCA 86

RESULT 4
US-10-475-851A-3
; Sequence 3, Application US/10475851A
; Publication No. US20040248114A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, Kazunari
; APPLICANT: WARASHINA, Tomoko
; APPLICANT: WARASHINA, Masaki
; APPLICANT: KAWASAKI, Hiroaki
; APPLICANT: HARA, Toshifumi
; APPLICANT: NOZAWA, Iwao
; TITLE OF INVENTION: Novel Maxizyme
; FILE REFERENCE: P24426
; CURRENT APPLICATION NUMBER: US/10/475,851A
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/JP02/04322
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-475-851A-3

Query Match   78.7%; Score 74.8; DB 18; Length 88;
Best Local Similarity   91.9%; Pred. No. 2.3e-18;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60
       |||||||||| |||||||| |||||||||||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGCGCGGAAACAAAGACA 86
       |||||||||||||||| | ||||||||
Db 61 UUCGAAACCGGGCGCGGCACUACAAAAACCA 86

RESULT 5
US-09-974-974-17
; Sequence 17, Application US/09974974
; Publication No. US20030013095A1
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; APPLICANT: Tomoko WARASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; TITLE OF INVENTION: target RNA by recognizing another molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,974
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 138
; TYPE: RNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNAVal T-MzL
US-09-974-974-17

Qy Best Local Similarity 78.7%; Score 74.8; DB 10; Length 138;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60

Qy 61 UUCGAAAACCGGGGCGGGGAAAACAAAAGACA 86
       |||||||||||||||| ||| |||
Db 61 UUCGAAAACCGGGGCACUACAAAAACCA 86

RESULT 6
US-10-361-028-52
; Sequence 52, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361,028
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US/09/704,525
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: JP 316133/1999
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 141
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
US-10-361-028-52

Query Match 78.7%; Score 74.8; DB 16; Length 141;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60

Qy 61 UUCGAAAACCGGGGCGGGGAAAACAAAAGACA 86
       |||||||||||||||| ||| |||
Db 61 UUCGAAAACCGGGGCACUACAAAAACCA 86

RESULT 7
US-10-361-028-49
; Sequence 49, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361,028
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US/09/704,525

; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: JP 316133/1999
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 142
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
US-10-361-028-50

Query Match 78.7%; Score 74.8; DB 16; Length 142;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60

Qy 61 UUCGAAAACCGGGGCGGGGAAAACAAAAGACA 86
       |||||||||||||||| ||| |||
Db 61 UUCGAAAACCGGGGCACUACAAAAACCA 86

RESULT 8
US-10-361-028-50
; Sequence 50, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361,028
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US/09/704,525
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: JP 316133/1999
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 142
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence of CPP Rz1
; OTHER INFORMATION: sequence of CPP Rz4
US-10-361-028-49

RESULT 9
US-10-361-028-51
; Sequence 51, Application US/10361028
; Publication No. US20030199471A1
; GENERAL INFORMATION:

```
;  APPLICANT: TAIRA, KAZUNARI
;  APPLICANT: WARASHINA, MASAKI
;  APPLICANT: KUWABARA, TOMOKO
;  APPLICANT: KAWASAKI, HIROAKI
;  TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
;  FILE REFERENCE: 081356/0151
;  CURRENT APPLICATION NUMBER: US/10/361,028
;  CURRENT FILING DATE: 2003-02-10
;  PRIOR APPLICATION NUMBER: US/09/704,525
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: JP 316133/1999
;  PRIOR FILING DATE: 1999-11-05
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 51
;  LENGTH: 142
;  TYPE: RNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
US-10-361-028-51

Qy  61 UUCGAAACCGGGCGCGGGAAACAAAGACA 86
       ||||||||||||||| | |||||||||
Db  61 UUCGAAACCGGGCACUACAAAAAACCA 86

Query Match      78.7%;     Score 74.8;   DB 16;   Length 142;
Best Local Similarity       91.9%;     Pred. No. 2.5e-18;
Matches  79;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy   1 ACCGUUGGUUUCCGUAGUGUGUAGUGUGUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60
       ||||||||||||||||||||||       ||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUGUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60

RESULT 10
US-10-361-028-53
;  Sequence 53, Application US/10361028
;  Publication No. US20030199471A1
;  GENERAL INFORMATION:
;  APPLICANT: TAIRA, KAZUNARI
;  APPLICANT: WARASHINA, MASAKI
;  APPLICANT: KUWABARA, TOMOKO
;  APPLICANT: KAWASAKI, HIROAKI
;  TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
;  FILE REFERENCE: 081356/0151
;  CURRENT APPLICATION NUMBER: US/10/361,028
;  CURRENT FILING DATE: 2003-02-10
;  PRIOR APPLICATION NUMBER: US/09/704,525
;  PRIOR FILING DATE: 2000-11-03
;  PRIOR APPLICATION NUMBER: JP 316133/1999
;  PRIOR FILING DATE: 1999-11-05
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 53
;  LENGTH: 142
;  TYPE: RNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
;                     sequence of CPP Rz3
US-10-361-028-53
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Db  61 UUCGAAACCGGGCACUACAAAAAACCA 86
       |||||||||||||| | |||||||||

RESULT 11
US-10-820-3
;  Sequence 3, Application US/10820820
;  Publication No. US20040198689A1
;  GENERAL INFORMATION:
;  APPLICANT: TAIRA, KAZUNARI
;  APPLICANT: OHKAWA, JUN
;  APPLICANT: KOSEKI, SHIORI
;  TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
;  TITLE OF INVENTION: NUCLEIC ACIDS
;  CURRENT APPLICATION NUMBER: US/10/820,820
;  CURRENT FILING DATE: 2004-04-09
;  PRIOR APPLICATION NUMBER: US/09/763,590
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: PCT/JP99/04718
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: JP 10/244755
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 3
;  LENGTH: 128
;  TYPE: RNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
US-10-820-820-3

Qy   1 ACCGUUGGUUUCCGUAGUGUGUAGUGUGUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60
       |||||||||||||||||||||       |||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUGUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60

Query Match      77.9%;     Score 74;   DB 18;   Length 128;
Best Local Similarity       93.9%;     Pred. No. 0;   Mismatches  5;   Indels  0;   Gaps  0;
Matches  77;  Conservative  0;

Qy  61 UUCGAAACCGGGCGCGGGAAACAAA 82
       ||||||||||||| |  |||||||
Db  61 UUCGAAACCGGGCACCCACACA 82
```

```
RESULT 12
US-10-820-1
;  Sequence 1, Application US/10820820
;  Publication No. US20040198689A1
;  GENERAL INFORMATION:
;  APPLICANT: TAIRA, KAZUNARI
;  APPLICANT: OHKAWA, JUN
;  APPLICANT: KOSEKI, SHIORI
;  TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
;  TITLE OF INVENTION: NUCLEIC ACIDS
;  FILE REFERENCE: 04853.0059-00000
;  CURRENT APPLICATION NUMBER: US/10/820,820
;  CURRENT FILING DATE: 2004-04-09
;  PRIOR APPLICATION NUMBER: US/09/763,590
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: PCT/JP99/04718
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: JP 10/244755
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 1
;  LENGTH: 135
;  TYPE: RNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
```

; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence of Rz2
US-10-820-820-1

Qy   1 ACCGUUGGUUUCCGUAGUGUGAGUGUAUCACGGUUCGCCUAACACGCGGAAAAGGUCCCCGG 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUGAGUGUAUCACGGUUCGCCUAACACGCGGAAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGCGGGAAACAA 81
         |||||||||||| |||
Db 61 UUCGAAACCGGGCCACUACAAA 81

RESULT 13
US-10-820-820-2
; Sequence 2, Application US2004019868A1
; Publication No. US2004019868A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/10/820,820
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US/09/763,590
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 2
; LENGTH: 141
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence of Rz3
US-10-820-820-2

Query Match   76.8%; Score 73; DB 18; Length 141;
Best Local Similarity   93.8%; Pred. No. 1.2e-17;
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUUCCGUAGUGUGAGUGUAUCACGGUUCGCCUAACACGCGGAAAAGGUCCCCGG 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUGAGUGUAUCACGGUUCGCCUAACACGCGGAAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGCGGGAAACAA 81
         |||||||||||| |||
Db 61 UUCGAAACCGGGCCACUACAAA 81

RESULT 14
US-10-820-820-5
; Sequence 5, Application US10820820
; Publication No. US2004019868A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/10/820,820
; CURRENT FILING DATE: 2004-04-09

Query Match   76.8%; Score 73; DB 18; Length 141;
Best Local Similarity   93.8%; Pred. No. 1.2e-17;
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUUCCGUAGUGUGAGUGUAUCACGGUUCGCCUAACACGCGGAAAAGGUCCCCGG 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUGAGUGUAUCACGGUUCGCCUAACACGCGGAAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGCGGGAAACAA 81
         |||||||||||| |||
Db 61 UUCGAAACCGGGCCACUACAAA 81

; PRIOR APPLICATION NUMBER: US/09/763,590
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 5
; LENGTH: 149
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence of Rz4
US-10-820-820-5

Query Match   73.5%; Score 69.8; DB 18; Length 149;
Best Local Similarity   97.3%; Pred. No. 2e-16;
Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUUCCGUAGUGUGAGUGUAUCACGGUUCGCCUAACACGCGGAAAAGGUCCCCGG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUGAGUGUAUCACGGUUCGCCUAACACGCGGAAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGC 73
         |||||||||||||
Db 61 UUCGAAACCGGGC 73

RESULT 15
US-10-820-820-7/c
; Sequence 7, Application US/10820820
; Publication No. US2004019868A1
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; TITLE OF INVENTION: NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/10/820,820
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US/09/763,590
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 7
; LENGTH: 113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence of an
; OTHER INFORMATION: antisense oligonucleotide linker
US-10-820-820-7

Query Match   70.3%; Score 66.8; DB 18; Length 113;
Best Local Similarity   71.4%; Pred. No. 2.6e-15;
Matches 50; Conservative 18; Mismatches 2; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUUCCGUAGUGUGAGUGUAUCACGGUUCGCCUAACACGCGGAAAAGGUCCCCGG 60
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Db   1 ACCGTTGGTTTCCGTAGTGTGAGTGTTATCACGTTCGCCTAACACGCGGAAAAGGTCCCCGG 60

Qy 61 UUCGAAACCG 70
         ::||||||||
Db 71 TTCGAAAGTCG 12

Qy 61 UUCGAAACCG 70
         :::|||| ||
Db 11 TTCGAAGTCG 2

us-10-820-820-4.rnpb

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: February 18, 2005, 21:34:12 ; Search time 2446 Seconds (without alignments) 1585.523 Million cell updates/sec

Title: US-10-820-820-4
Perfect score: 95
Sequence: 1 accguuggguuccguaguguu........aaacaaagacagucgcuuuu 95

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 4555487 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 41414866

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Maximum DB seq length: 150

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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21: /cgn2_6/ptcdata/1/pna/US093B_COMB.seq:*
22: /cgn2_6/ptcdata/1/pna/US094_COMB.seq:*
23: /cgn2_6/ptcdata/1/pna/US095A_COMB.seq:*
24: /cgn2_6/ptcdata/1/pna/US095B_COMB.seq:*
25: /cgn2_6/ptcdata/1/pna/US095C_COMB.seq:*
26: /cgn2_6/ptcdata/1/pna/US095D_COMB.seq:*
27: /cgn2_6/ptcdata/1/pna/US096A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	95	100.0	95	32	US-09-718-098-15	Sequence 15, Appl
3	95	100.0	95	32	US-10-361-028-8	Sequence 8, Appli
4	95	100.0	63	53	US-10-820-820-4	Sequence 4, Appli
5	95	100.0	63	53	US-09-623-932-3	Sequence 3, Appli
6	74.8	78.7	88	28	US-09-623-932A-3	Sequence 3, Appli
7	74.8	78.7	88	44	US-09-974-974-5	Sequence 5, Appli
8	74.8	78.7	88	55	US-10-475-851A-3	Sequence 3, Appli
9	74.8	78.7	56	32	US-10-512-386-1	Sequence 1, Appli
10	74.8	78.7	91	32	US-09-718-098-16	Sequence 16, Appl
11	74.8	78.7	28	28	US-09-623-932A-20	Sequence 20, Appl
12	74.8	78.7	128	28	US-09-623-932A-18	Sequence 18, Appl
13	74.8	78.7	137	45	US-09-984-198A-2	Sequence 2, Appli
14	74.8	78.7	138	44	US-09-974-974-17	Sequence 17, Appl
15	74.8	78.7	141	32	US-09-704-525-52	Sequence 52, Appl
16	74.8	78.7	141	53	US-10-361-028-52	Sequence 52, Appl
17	74.8	78.7	142	32	US-09-704-525-49	Sequence 49, Appl
18	74.8	78.7	142	32	US-09-704-525-50	Sequence 50, Appl
19	74.8	78.7	142	32	US-09-704-525-51	Sequence 51, Appl
20	74.8	78.7	142	53	US-10-361-028-49	Sequence 49, Appl
21	74.8	78.7	142	53	US-10-361-028-50	Sequence 50, Appl
22	74.8	78.7	142	53	US-10-361-028-51	Sequence 51, Appl
23	74.8	78.7	142	53	US-10-361-028-51	Sequence 51, Appl
24	74.8	78.7	142	53	US-10-361-028-53	Sequence 53, Appl
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26	76.8	73	135	63	US-10-820-820-3	Sequence 3, Appl
27	76.8	73	141	63	US-10-820-820-2	Sequence 2, Appl
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29	70.3	66.8	113	63	US-10-820-820-5	Sequence 5, Appl
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31	66.3	63	64	2	PCT-US03-40292-57	Sequence 57, Appl
32	66.3	63	62		US-09-047-925-3336	Sequence 3336, Appl
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36	42.1	40	73	79	US-60-615-573-3	Sequence 3, Appl
37	40.8	38.8	73	22	US-60-450-969-3090	Sequence 3090, App
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39	40.4	38.4	73	79	US-60-615-573-10841	Sequence 10841, A
40	40.4	38.4	138	22	US-09-450-969-2465	Sequence 2465, Ap
41	40.4	38.4	138	62	US-09-724-972A-2465	Sequence 2465, Ap
42	37.1	35.2	73	64	US-10-857-625-384	Sequence 384, App
43	37.1	35.2	73	64	US-10-857-625-404	Sequence 404, App
44	37.1	35.2	73	64	US-10-857-625-407	Sequence 407, App
45	37.1	35.2	73	64	US-10-859-198-3224	Sequence 3224, Ap

ALIGNMENTS

RESULT 1
US-09-704-525-8
Sequence 8, Application US/09704525
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/09/704,525
; CURRENT FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: JP 316133/1999
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 95
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
; OTHER INFORMATION: sequence of the transcript of the human placental tRNAval
US-09-704-525-8

Query Match 100.0%; Score 95; DB 32; Length 95;
Best Local Similarity 100.0%; Pred. No. 4e-25;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Sequence 15, Application US/09718098
; GENERAL INFORMATION:
; APPLICANT: TANAKA, MANAMI
; TITLE OF INVENTION: RIBOZYMES TARGETING BRADEION TRANSCRIPTS AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 081356/0155
; CURRENT APPLICATION NUMBER: US/09/718,098
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 95
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNA(val) promoter
US-09-718-098-15

Query Match 100.0%; Score 95; Pred. No. 4e-25;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11/22/05   X

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Qy 61 UUCGAAAACCGGCGGGCGGAAACAAAAGACAGUCGCUUU 95
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US-10-361-028-8

Sequence 8, Application US/1361028
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/10/361,028
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: US/09/704,525
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: JP 316133/1999
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 95
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
; OTHER INFORMATION: sequence of the transcript of the human placental tRNAVal
US-10-361-028-8

Qy Query Match   100.0%;   Score 95; DB 53;   Length 95;
Best Local Similarity 100.0%;   Pred. No. 4e-25;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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Sequence 4, Application US/10820820
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: OHKAWA, JUN
; APPLICANT: KOSEKI, SHIORI
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR TRANSCRIPTION OF FUNCTIONAL
; NUCLEIC ACIDS
; FILE REFERENCE: 04853.0059-00000
; CURRENT APPLICATION NUMBER: US/10/820,820
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US/09/763,590
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: PCT/JP99/04718
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: JP 10/244755
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 95
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence of the transcript of human placental tRNA Val
US-10-820-820-4

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Best Local Similarity 100.0%;   Pred. No. 4e-25;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-623-932-3
Sequence 3, Application US/09623932
; GENERAL INFORMATION:
; APPLICANT: DIRECTOR-GENERAL OF INDUS. SCIENCE & TECH. AGENCY
; APPLICANT: TAISHO PHARMACEUTICAL CO., LTD.
; TITLE OF INVENTION: NUCLEIC ACID ENZYME HAVING ALLOSTERIC RNA-CLEAVING
; ACTIVITY ON TARGET RNA
; FILE REFERENCE: Q60764
; CURRENT APPLICATION NUMBER: US/09/623,932
; CURRENT FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence of tRNAVal
US-09-623-932-3

Qy Query Match   78.7%;   Score 74.8; DB 28;   Length 88;
Best Local Similarity 91.9%;   Pred. No. 1.8e-17;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 61 UUCGAAACCGGGCGGGGAAACAAAGACA 86
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Db 61 UUCGAAACCGGGCCACUACAAAAAACCA 86

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US-09-623-932A-3
Sequence 3, Application US/09623932A
; GENERAL INFORMATION:
; APPLICANT: Taisho Pharmaceutical Co., Ltd.
; APPLICANT: Japan as rep'd by Secretary of Agency of Industrial Science and Technol.
; TITLE OF INVENTION: Nucleic acid enzyme having allosteric RNA-cleaving activity on
; FILE REFERENCE: Q60764
; CURRENT APPLICATION NUMBER: US/09/623,932A
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: JP 60969/1998
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: JP 311098/1998
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: PCT/JP99/01187
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of tRNAVal
US-09-623-932A-3

Qy Query Match   78.7%;   Score 74.8; DB 28;   Length 88;
Best Local Similarity 91.9%;   Pred. No. 1.8e-17;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db    1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60

Qy   61 UUCGAAAACCGGGCGCGGGAAAACAAAGACA 86
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Db   61 UUCGAAAACCGGGCACUACAAAAAACCA 86
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RESULT 7
US-09-974-974-5
; Sequence 5, Application US/09974974
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; APPLICANT: Tomoko WARASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; TITLE OF INVENTION: target RNA by recognizing another molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,974
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
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; SEQ ID NO 5
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNAVal promoter sequence

US-09-974-974-5

Query Match   78.7%; Score 74.8; DB 44; Length 88;
Best Local Similarity   91.9%; Pred. No.1.8e-17;
Matches   79; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

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Db    1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60

Qy   61 UUCGAAAACCGGGCGCGGGAAAACAAAGACA 86
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Db   61 UUCGAAAACCGGGCACUACAAAAAACCA 86
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RESULT 8
US-10-475-851A-3
; Sequence 3, Application US/10475851A
; GENERAL INFORMATION:
; APPLICANT: TAIRA, Kazunari
; APPLICANT: WARASHINA, Tomoko
; APPLICANT: WARASHINA, Masaki
; APPLICANT: KAWASAKI, Hiroaki
; APPLICANT: HARA, Toshifumi
; APPLICANT: NOZAWA, Iwao
; TITLE OF INVENTION: Novel Maxizyme
; FILE REFERENCE: P24426
; CURRENT APPLICATION NUMBER: US/10/475,851A
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: PCT/JP02/04322
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 3
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Homo sapiens

US-10-475-851A-3

Query Match   78.7%; Score 74.8; DB 55; Length 88;
Best Local Similarity   91.9%; Pred. No.1.8e-17;
Matches   79; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

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Qy    1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60

Qy   61 UUCGAAAACCGGGCGCGGGAAAACAAAGACA 86
        ||||||||||  ||||  || ||||||||||
Db   61 UUCGAAAACCGGGCACUACAAAAAACCA 86
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RESULT 9
US-10-512-386-1
; Sequence 1, Application US/10512386
; GENERAL INFORMATION:
; APPLICANT: NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR STEM-LOOP RNA MOLECULES HAVING RNAi EFFEC
; FILE REFERENCE: GFU-A02031P
; CURRENT APPLICATION NUMBER: US/10/512,386
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: JP 2002-127089
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: JP 2003-4706
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/449,860
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 1
; LENGTH: 88
; TYPE: RNA
; ORGANISM: Homo sapiens

US-10-512-386-1

Query Match   78.7%; Score 74.8; DB 56; Length 88;
Best Local Similarity   91.9%; Pred. No.1.8e-17;
Matches   79; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

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Qy    1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60

Qy   61 UUCGAAAACCGGGCGCGGGAAAACAAAGACA 86
        ||||||||||  ||||  || ||||||||||
Db   61 UUCGAAAACCGGGCACUACAAAAAACCA 86
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RESULT 10
US-09-718-098-16
; Sequence 16, Application US/09718098
; GENERAL INFORMATION:
; APPLICANT: TANAKA, MANAMI
; TITLE OF INVENTION: RIBOZYMES TARGETING BRADEION TRANSCRIPTS AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 081356/0155
; CURRENT APPLICATION NUMBER: US/09/718,098
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 16
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A mutant tRNA(Val)
; OTHER INFORMATION: promoter

US-09-718-098-16

Query Match   78.7%; Score 74.8; DB 32; Length 91;
Best Local Similarity   70.9%; Pred. No.1.8e-17;
Matches   61; Conservative   18; Mismatches   7; Indels   0; Gaps   0;

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Qy    1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
        |||| |||| ||||:|||:||:||:|||||||:|:|||||||||||:|||||:||||||||
Db    1 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTGCCTAACACGGGAAAGGTCCCCGG 60
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Qy 61 UUCGAAACCGGGCGCGGAAACAAGAGACA 86
Db 61 UUCGAAACCGGGCGACUACAAAAAACCA 86

RESULT 11
US-09-623-932A-20
; Sequence 20, Application US/0962932A-20
; GENERAL INFORMATION:
; APPLICANT: Taisho Pharmaceutical Co., Ltd.
; APPLICANT: Japan as rep'd by Secretary of Agency of Industrial Science and Technolog
; TITLE OF INVENTION: Nucleic acid enzyme having allosteric RNA-cleaving activity on ta
; FILE REFERENCE: Q60764
; CURRENT FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: US/09/623,932A
; PRIOR APPLICATION NUMBER: JP 60969/1998
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: JP 311098/1998
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: PCT/JP99/01187
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 128
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Component of tRNAval-MzR
US-09-623-932A-20

Query Match   Best Local Similarity   91.9%;   Score 74.8; DB 28; Length 128;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy   1 ACGGUUGGUUUCCGUAGUGUAGUGUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCCGG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACGGUUGGUUUCCGUAGUGUAGUGUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGCGCGGAAACAAGAGACA 86
Db 61 UUCGAAACCGGGCGACUACAAAAAACCA 86

RESULT 12
US-09-623-932A-18
; Sequence 18, Application US/0962932A
; GENERAL INFORMATION:
; APPLICANT: Taisho Pharmaceutical Co., Ltd.
; APPLICANT: Japan as rep'd by Secretary of Agency of Industrial Science and Technolog
; TITLE OF INVENTION: Nucleic acid enzyme having allosteric RNA-cleaving activity on ta
; FILE REFERENCE: Q60764
; CURRENT FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: US/09/623,932A
; PRIOR APPLICATION NUMBER: JP 60969/1998
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: JP 311098/1998
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: PCT/JP99/01187
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 135
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Component of tRNAval-MzL
US-09-623-932A-18

Query Match   Best Local Similarity   91.9%;   Score 74.8; DB 28; Length 135;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCCGG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGCGCGGAAACAAGAGACA 86
Db 61 UUCGAAACCGGGCGACUACAAAAAACCA 86

RESULT 13
US-09-984-198A-2
; Sequence 2, Application US/09984198A
; GENERAL INFORMATION:
; APPLICANT: Taira, Kazunari
; APPLICANT: Sano, Masayuki
; TITLE OF INVENTION: METHODS FOR SELECTING HIGHLY FUNCTIONAL NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: WITHIN CELLS
; FILE REFERENCE: 4853.0080-00
; CURRENT APPLICATION NUMBER: US/09/984,198A
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 331347/2000
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 137
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70)..(91)
; OTHER INFORMATION: 22mer random sequence
US-09-984-198A-2

Query Match   Best Local Similarity   91.9%;   Score 74.8; DB 45; Length 137;
Matches 79; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCCGG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCCGG 60

Qy 61 UUCGAAACCGGGCGCGGAAACAAGAGACA 86
Db 61 UUCGAAACCGGGCGACUACAAAAAACCA 86

RESULT 14
US-09-974-974-17
; Sequence 17, Application US/09974974
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; APPLICANT: Tomoko WARASHINA
; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; TITLE OF INVENTION: target RNA by recognizing another molecule
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,974
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 138
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tRNAVal T-MzL

US-09-974-974-17

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Query Match        78.7%;   Score 74.8;  DB 44;   Length 138;
Best Local Similarity  91.9%;   Pred. No. 2e-17;
Matches  79;  Conservative   0;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    1 ACCGUUGGUUUCCGUAGUGUGAGUGUGUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCGG  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ACCGUUGGUUUCCGUAGUGUGGUUAUCCACGUUCGCCUAACACGCGAAAAGGUCCCCGG  60

Qy   61 UUCGAAACCGGGGCGGGGAAAACAAAAGACA  86
        ||||||||||||||||    ||  |||  ||
Db   61 UUCGAAACCGGGGCACUACAAAAAACCA  86
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RESULT 15
US-09-704-525-52
; Sequence 52, Application US/09704525
; GENERAL INFORMATION:
; APPLICANT: TAIRA, KAZUNARI
; APPLICANT: WARASHINA, MASAKI
; APPLICANT: KUWABARA, TOMOKO
; APPLICANT: KAWASAKI, HIROAKI
; TITLE OF INVENTION: FUNCTIONAL CHIMERIC MOLECULES CAPABLE OF SLIDING
; FILE REFERENCE: 081356/0151
; CURRENT APPLICATION NUMBER: US/09/704,525
; CURRENT FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: JP 316133/1999
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.1
;
; SEQ ID NO 52
;   LENGTH: 141
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: the nucleotide
;   OTHER INFORMATION: sequence of CPP Rz4
US-09-704-525-52

```
Query Match        78.7%;   Score 74.8;  DB 32;   Length 141;
Best Local Similarity  91.9%;   Pred. No. 2e-17;
Matches  79;  Conservative   0;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    1 ACCGUUGGUUUCCGUAGUGUGAGUGUGUUAUCACGUUCGCCUAACACGCGAAAAGGUCCCGG  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ACCGUUGGUUUCCGUAGUGUGGUUAUCCACGUUCGCCUAACACGCGAAAAGGUCCCCGG  60

Qy   61 UUCGAAACCGGGGCGGGGAAAACAAAAGACA  86
        ||||||||||||||||    ||  |||  ||
Db   61 UUCGAAACCGGGGCACUACAAAAAACCA  86
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Search completed: February 18, 2005, 23:15:43
Job time : 2448 secs